

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 22, 2006, 18:51:30 ; Search time 194 Seconds  
(without alignments)  
525.563 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTWRRHVRLLFTSLLQII.....PSVLOQERRPCGPGPLGHRL 223

Scoring table: OLIIGO  
Gapext 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 6

Total number of hits satisfying chosen parameters: 14456

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq 8 : \*

- 1: geneseqP1980s:\*
- 2: geneseqP1990s:\*
- 3: geneseqP2000s:\*
- 4: geneseqP2001s:\*
- 5: geneseqP2002s:\*
- 6: geneseqP2003s:\*
- 7: geneseqP2003bs:\*
- 8: geneseqP2004s:\*
- 9: geneseqP2005s:\*
- 10: geneseqP2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	223	100.0	223	8	ADO05060		Ado05060 Human cri
2	223	100.0	229	4	AAU18122		AAu18122 Novel hum
3	223	100.0	229	4	AAU17028		AAu17028 Human nov
4	223	100.0	229	4	ABB10300		Abb10300 Human cDN
5	223	100.0	229	4	AAU19904		AAu19904 Novel hum
6	223	100.0	229	5	ABJ05149		Abj05149 Novel hum
7	223	100.0	229	5	ABP66887		Abp66887 Human pol
8	187	83.9	223	5	ABB90136		Abb90136 Human pol
9	187	83.9	223	6	ABU56711		Abu56711 Lung canc
10	187	83.9	223	7	ADN39104		Adn39104 Cancer/an
11	187	83.9	223	7	ADN39975		Adn39975 Cancer/an
12	187	83.9	223	9	ADY85563		Ady85563 Human Cri
13	187	83.9	231	4	AAU16357		AAu16357 Human nov
14	149	66.8	230	2	AAW09111		Aaw09111 Human cri
15	145	65.0	223	5	AGG77914		AGG77914 Human cry
16	15	6.7	202	9	ADY85962		Ady85962 Murine Cr
17	14	6.3	14	4	AAM00665		Aam00665 Human pro
18	8	3.6	60	4	AAM05349		Aam05349 Human fo
19	8	3.6	64	4	AAM06722		Aam06722 Human fo
20	8	3.6	120	4	AAO10911		Aao10911 Human pol
21	8	3.6	158	4	AAM99763		Aam99763 Human exc
22	8	3.6	180	4	AAM99763		Aam99763 Human pol
23	8	3.6	180	4	AAM42398		Aam42398 Human pol

OS Homo sapiens.

XX

PN US2004086967-A1.

XX

PD 06-MAY-2004.

XX

PP 22-SEP-2003; 2003US-00665602.

XX

PR 06-JUN-1995; 95US-00471371.

XX

PR 09-SEP-1999; 99US-00393023.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Meissner PS, Coleman TA,

XX

DR WPI; 2004-356201/33.

DR N-PSDB; ADO05059.

XX

PS Claim 12; SEQ ID NO 2; 19pp; English.

XX

CC The invention provides cryptin growth factor (CGF) polypeptides and their encoding polynucleotides. The invention is useful for wound healing and tissue regeneration, stimulating implant fixation, angiogenesis and for treating and preventing neoplasia such as tumour. The invention is also useful in gene therapy. The present sequence is human cryptin growth factor (CGF) protein.

CC

CC

XX

SQ Sequence 223 AA;

## ALIGNMENTS

24	8	3.6	180	4	AAM42578	Human kid
25	8	3.6	ABM8084	7	ABM8084	Rice abio
26	8	3.6	334	8	ADU02861	Novel hum
27	8	3.6	363	7	ABO69270	Pseudomon
28	8	3.6	420	6	ABU1822	Human MDD
29	8	3.6	575	8	ADY08754	Plant ful
30	8	3.6	575	8	ADY12991	Plant ful
31	8	3.6	788	8	ADY08040	Plant ful
32	8	3.6	788	8	AD05178	Protein #
33	8	3.6	1230	5	AAO21533	Human mit
34	8	3.6	1230	7	ADE61957	Human Pro
35	8	3.6	1230	7	ADD45964	Human Pro
36	8	3.6	1253	4	ABG23851	Novel hum
37	8	3.6	1718	5	AAE26420	Human tra
38	8	3.6	2523	8	ADL26915	Xenopus s
39	7	3.1	21	9	ADY55161	G protein
40	7	3.1	22	7	ADE28537	Human CD1
41	7	3.1	24	5	ABB74254	Fusogenic
42	7	3.1	27	4	AAB03135	Human gen
43	7	3.1	30	9	ADZ77602	Human MHC
44	7	3.1	33	9	ADY28315	Novel Erb
45	7	3.1	38	4	AAO03363	Human pol

## RESULT 1

ADO05060

ID ADO05060 standard; protein; 223 AA.

XX

AC ADO05060;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human cryptin growth factor (CGF) protein.

XX

KW Cryptin growth factor; CGF; wound healing; tissue regeneration; implant fixation; angiogenesis; neoplasia; tumour; gene therapy; human.

XX

OS Homo sapiens.

XX

PN US2004086967-A1.

XX

PD 06-MAY-2004.

XX

PP 22-SEP-2003; 2003US-00665602.

XX

PR 06-JUN-1995; 95US-00471371.

XX

PR 09-SEP-1999; 99US-00393023.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Meissner PS, Coleman TA,

XX

DR WPI; 2004-356201/33.

DR N-PSDB; ADO05059.

XX

PS Claim 12; SEQ ID NO 2; 19pp; English.

XX

CC The invention provides cryptin growth factor (CGF) polypeptides and their encoding polynucleotides. The invention is useful for wound healing and tissue regeneration, stimulating implant fixation, angiogenesis and for treating and preventing neoplasia such as tumour. The invention is also useful in gene therapy. The present sequence is human cryptin growth factor (CGF) protein.

CC

CC

XX

SQ Sequence 223 AA;

Query Match 100.0%; score 223; DB 8; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1; 4e-195; Indels 0; Gaps 0;  
 Matches 223; Conservative 0; Mismatches 0;

Qy 1 MTWRRHVRLLFTVSLAQIINLGNSYQREKHNGRGEVTKVATQKHRQSPLENNTSSHFGE 60  
 Db 1 MTWRRHVRLLFTVSLAQIINLGNSYQREKHNGRGEVTKVATQKHRQSPLENNTSSHFGE 60

Qy 61 VIGSAEGNGPPEEPYPSRAFEGEGASARPCCRNGGTCVIGSFCVCPAHTFGRYCEHDFR 120  
 Db 61 VIGSAEGNGPPEEPYPSRAFEGEGASARPCCRNGGTCVIGSFCVCPAHTFGRYCEHDFR 120

Qy 121 SEC5ALENGAWTTLRACHLRCITGAHLHCLPLQTPDRCDPKDPLASHAGPSAGAPSILL 180  
 Db 121 SEC5ALENGAWTTLRACHLRCITGAHLHCLPLQTPDRCDPKDPLASHAGPSAGAPSILL 180

Qy 181 LLPCALLHLLRDPAPAHRSLYPSVLQERRPGPGLGHRL 223  
 Db 181 LLPCALLHLLRDPAPAHRSLYPSVLQERRPGPGLGHRL 223

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RESULT 2

AAU18122 standard; protein; 229 AA.

XX ID AAU18122 (first entry)

XX Novel human uterine motility-association polypeptide #29.

DE Human; uterine motility-association disorder; uterus; pregnancy; labour; menstrual cycle; gene therapy.

XX KW Human; uterine motility-association disorder; uterus; pregnancy; labour; menstrual cycle; gene therapy.

XX Homo sapiens.

XX WO200155201-A1.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001317.

XX 31-JAN-2000; 2000US-01790659P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUL-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-021647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-025213P.

PR 14-AUG-2000; 2000US-02525214P.

PR 26-JUL-2000; 2000US-0220964P.

PR 26-JUL-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-025267P.

PR 14-AUG-2000; 2000US-0252568P.

PR 14-AUG-2000; 2000US-0255270P.

PR 14-AUG-2000; 2000US-025547P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 01-SEP-2000; 2000US-022928P.

PR 01-SEP-2000; 2000US-0229333P.

PR 01-SEP-2000; 2000US-023124P.

PR 01-SEP-2000; 2000US-0231243P.

PR 05-SEP-2000; 2000US-022950P.

PR 06-SEP-2000; 2000US-0231413P.

PR 06-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0232081P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232400P.

PR 08-SEP-2000; 2000US-0232401P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

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PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234224P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235444P.

PR 27-SEP-2000; 2000US-0235814P.

PR 27-SEP-2000; 2000US-0235816P.

PR 29-SEP-2000; 2000US-0236321P.

PR 29-SEP-2000; 2000US-0236377P.

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PR 02-OCT-2000; 2000US-023703P.

PR 02-OCT-2000; 2000US-0237030P.

PR 02-OCT-2000; 2000US-0237031P.

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PR 02-OCT-2000; 2000US-0237039P.

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PR 13-OCT-2000; 2000US-023935P.

PR 13-OCT-2000; 2000US-023937P.

PR 20-OCT-2000; 2000US-0240961P.

PR 20-OCT-2000; 2000US-0241221P.

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PR 20-OCT-2000; 2000US-0241766P.

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PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0244614P.

PR 08-NOV-2000; 2000US-0246475P.

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PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.

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PR 08-NOV-2000; 2000US-0246533P.

PR 08-NOV-2000; 2000US-0246534P.

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PR 08-NOV-2000; 2000US-0246538P.

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PR	17-NOV-2000;	2000US-0245207P.	Db	127	SECCALENGCAWTILRACHILCRCIFGALHCLPLQTPDRCDPKDPLASHAHPGSAGGAPSLL	186
PR	17-NOV-2000;	2000US-0245208P.				
PR	17-NOV-2000;	2000US-0245210P.	Qy	181	LLPCALLRLRPPAPAHRSVLPSVLQRERRPGRPGLGHRL	223
PR	17-NOV-2000;	2000US-0245211P.	Db	187	LLPCALLRLRPPAPAHRSVLPSVLQRERRPGRPGLGHRL	229
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PR	08-DEC-2000;	2000US-0251479P.				
PR	05-JAN-2001;	2001US-0259678P.				
XX	(HUMA-)	HUMAN GENOME SCI INC.				
PA						
PA						
PI	2001-488777/53.					
XX	WPI: AAS28964.					
DR	N-PSDB; AAS28964.					
XX	The present invention relates to the isolation of novel human uterine					
CC	motility-association polypeptides, and cDNA (AAS28936-AAS8994) and					
CC	genomic sequences encoding for these polypeptides. The sequences of the					
CC	invention are useful in the diagnosis, treatment, prevention and/or					
CC	prognosis of diseases associated with uterine motility such as pregnancy					
CC	and labour, and menstrual disorders. The polypeptide sequences of the					
CC	invention are also useful in gene therapy. AAU1094-AAU1852 represent					
CC	novel human uterine motility-association polypeptides. Note: The sequence					
CC	data for this patent did not form part of the printed specification, but					
CC	was obtained in electronic format directly from WIPO at					
CC	ftp.wipo.int/pub/published_pct_sequences					
XX	Sequence 229 AA;					
SQ	Query Match 100.0%; Score 223; DB 4; Length 229;					
	Best Local Similarity 100.0%; Pred. No. 1.5e-19;					
	Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MTWRHHVRLLFTVSLQIINLGNSYQREKHNNGRGEVTKVATORKHRQSPLNMTSSHFGE	60			
Db	7	MTWRHHVRLLFTVSLQIINLGNSYQREKHNNGRGEVTKVATORKHRQSPLNMTSSHFGE	66			
	Query Match 100.0%; Score 223; DB 4; Length 229;					
	Best Local Similarity 100.0%; Pred. No. 1.5e-19;					
	Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	61	VTGSAEKGWPEEPLPYSRAGEGASARPRCCRNGETCVLGSFCVCPAHTGRCYCEHDQR	120			
Db	67	VTGSAEKGWPEEPLPYSRAGEGASARPRCCRNGETCVLGSFCVCPAHTGRCYCEHDQR	126			





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PR	17-NOV-2000;	2000US-0249215P.							
PR	17-NOV-2000;	2000US-0249216P.							
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PR	17-NOV-2000;	2000US-0249218P.							
PR	17-NOV-2000;	2000US-0249244P.							
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PR	05-DEC-2000;	2000US-0246719P.							
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PR	08-DEC-2000;	2000US-0241856P.							
PR	08-DEC-2000;	2000US-0241868P.							
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PR	08-DEC-2000;	2000US-0241989P.							
PR	08-DEC-2000;	2000US-0241990P.							
PR	11-DEC-2000;	2000US-0244097P.							
PR	05-JAN-2001;	2001US-0249678P.							
XX	(HUMA-) HUMAN GENOME SCI INC.								
PA	Rosen CA, Barash SC, Ruben SM;								
PA	WPTI; 2001-4-78161/51.								
DR	N-FSDB; ABA06522.								
XX	Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition.								
XX	Claim 11; SEQ ID NO 608; 859pp + Sequence Listing; English.								
CC	The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a protein of the invention								
XX	Sequence 229 AA;								
Query	Match	100.0%	Score	223;	DB	4;	Length	229;	
Best Local	Similarity	100.0%	;	No. 1.	Se-195;	Indels	0;	Gaps	0;
Matches	223;	Conservative	0;	Mismatches	0;				
Dy	1	MTWRRHVRLLFTVSLAQIQLINGLNSYQREKHNRRGERGTVKATQKHSRPLNTSSHGE	60	PR	22-AUG-2000;	2000US-0225113P	PR	14-AUG-2000;	2000US-024886P
Db	7	MTWRRHVRLLFTVSLAQIQLINGLNSYQREKHNRRGERGTVKATQKHSRPLNTSSHGE	66	PR	07-JUL-2000;	2000US-0225135P	PR	30-JUN-2000;	2000US-0220963P
Dy	61	VTGSAEGNGPPEEPPLYSRAFGEGASARPRCCRNGGTCVLSFCVCPAHTFTGRYCEHDQRR	120	PR	14-AUG-2000;	2000US-0224519P	PR	14-AUG-2000;	2000US-0224519P
Db	67	VTGSAEGNGPPEEPPLYSRAFGEGASARPRCCRNGGTCVLSFCVCPAHTFTGRYCEHDQRR	126	PR	14-AUG-2000;	2000US-0225214P	PR	14-AUG-2000;	2000US-0225266P
Dy	121	SECCALEHGAWTLRACHLRCIFQALHCLPQDFPRCDPKDFLASHAIGPSAGAPSLL	180	PR	31-SEP-2000;	2000US-0222287P	PR	01-SEP-2000;	2000US-0229343P
Db	127	SECCALEHGAWTLRACHLRCIFQALHCLPQDFPRCDPKDFLASHAIGPSAGAPSLL	186	PR	01-SEP-2000;	2000US-0222287P	PR	01-SEP-2000;	2000US-0229344P
Dy	181	LIPCALLHLRLLRPDAPAHRSLSVSVLQERRPGRGPGLGHRL	223	PR	08-SEP-2000;	2000US-0231243P	PR	08-SEP-2000;	2000US-0231244P
Db	187	LIPCALLHLRLLRPDAPAHRSLSVSVLQERRPGRGPGLGHRL	229	PR	08-SEP-2000;	2000US-0231413P	PR	08-SEP-2000;	2000US-0231414P
Dy	190	DAU19904	229	PR	08-SEP-2000;	2000US-0232080P	PR	08-SEP-2000;	2000US-0231968P
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RESULT 5  
AAU19904  
AAU19904 standard: mrmrain: 229 AA



OS	Host	Species	Strain	Collection Date	Collection Locality
OS	XXX	USSP	US2002086330-A1.		
OS	XXX	SPN			
OS	XXX	IPD			
OS	XXX	IPD	04-JUL-2002.		
OS	XXX	PP	17-JAN-2001;	2001US-00764893.	
OS	XXX	PP	31-JAN-2000;	2000US-0179065P.	
OS	XXX	PR	04-FEB-2000;	2000US-0180628P.	
OS	XXX	PR	04-FEB-2000;	2000US-0184886P.	
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OS	XXX	PR	11-JUL-2000;	2000US-0217487P.	
OS	XXX	PR	11-JUL-2000;	2000US-0217496P.	
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OS	XXX	PR	26-JUL-2000;	2000US-0220964P.	
OS	XXX	PR	14-AUG-2000;	2000US-0224518P.	
OS	XXX	PR	14-AUG-2000;	2000US-0224519P.	
OS	XXX	PR	14-AUG-2000;	2000US-0225267P.	
OS	XXX	PR	14-AUG-2000;	2000US-0225268P.	
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OS	XXX	PR	14-AUG-2000;	2000US-0225757P.	
OS	XXX	PR	22-AUG-2000;	2000US-0225758P.	
OS	XXX	PR	30-AUG-2000;	2000US-0226868P.	
OS	XXX	PR	01-SEP-2000;	2000US-02288924P.	
OS	XXX	PR	01-SEP-2000;	2000US-0229287P.	
OS	XXX	PR	01-SEP-2000;	2000US-0229343P.	
OS	XXX	PR	01-SEP-2000;	2000US-0229344P.	
OS	XXX	PR	01-SEP-2000;	2000US-0229345P.	
OS	XXX	PR	05-SEP-2000;	2000US-0229509P.	
OS	XXX	PR	05-SEP-2000;	2000US-0229513P.	
OS	XXX	PR	21-SEP-2000;	2000US-0231413P.	
OS	XXX	PR	21-SEP-2000;	2000US-024223P.	
OS	XXX	PR	25-SEP-2000;	2000US-024274P.	
OS	XXX	PR	27-SEP-2000;	2000US-024997P.	
OS	XXX	PR	02-OCT-2000;	2000US-025834P.	
OS	XXX	PR	02-OCT-2000;	2000US-026327P.	
OS	XXX	PR	29-SEP-2000;	2000US-026367P.	
OS	XXX	PR	29-SEP-2000;	2000US-026368P.	
OS	XXX	PR	02-OCT-2000;	2000US-026369P.	
OS	XXX	PR	13-OCT-2000;	2000US-026370P.	
OS	XXX	PR	20-OCT-2000;	2000US-026802P.	
OS	XXX	PR	20-OCT-2000;	2000US-027037P.	
OS	XXX	PR	02-OCT-2000;	2000US-027038P.	
OS	XXX	PR	02-OCT-2000;	2000US-027039P.	
OS	XXX	PR	02-OCT-2000;	2000US-027040P.	
OS	XXX	PR	13-OCT-2000;	2000US-027935P.	
OS	XXX	PR	20-OCT-2000;	2000US-0240960P.	
OS	XXX	PR	20-OCT-2000;	2000US-0241785P.	
OS	XXX	PR	01-NOV-2000;	2000US-0241809P.	
OS	XXX	PR	17-NOV-2000;	2000US-0249299P.	
OS	XXX	PR	08-DEC-2000;	2000US-0251856P.	
OS	XXX	PR	08-DEC-2000;	2000US-0251868P.	
OS	XXX	PR	08-DEC-2000;	2000US-0251869P.	

(ROSE) ROSEN C A.  
(RUBE) RUBEN S M.  
(BARA) BARASH S C.  
Rosen CA, Ruben SM, Barash SC;  
WPI: 2002-665432/71.

Novel polypeptide useful for diagnosis, prognosis, prevention, and treatment of immune, hyperproliferative, renal, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.

Disclosure: Page 268-269; 35pp; English.

Query Match	Start Local Similarity	End Local Similarity	Start Matchees	End Matchees	Score	DB	Length	Pred. No.	Missmatches	Indels	Gaps	0
1 MTWIRHVRLLFTVSLAQIQLINLGNSYQREKHNGGREGIVTKVATQHROSPINWTSFHFGE	100.0%	100.0%	223	229	60	5	229					
2 MTWIRHVRLLFTVSLAQIQLINLGNSYQREKHNGGREGIVTKVATQHROSPINWTSFHFGE	100.0%	100.0%	156	195	66	5	156					
3 MTWIRHVRLLFTVSLAQIQLINLGNSYQREKHNGGREGIVTKVATQHROSPINWTSFHFGE	100.0%	100.0%	156	195	66	5	156					
4 VTGSLEGWGPBPEPLYSRAFEGASARPRCCRNGTCVLGSFCVCPAHTGTYCCHDQRR	100.0%	100.0%	156	195	120	5	120					
5 VTGSLEGWGPBPEPLYSRAFEGASARPRCCRNGTCVLGSFCVCPAHTGTYCCHDQRR	100.0%	100.0%	156	195	126	5	126					
6 VTGSLEGWGPBPEPLYSRAFEGASARPRCCRNGTCVLGSFCVCPAHTGTYCCHDQRR	100.0%	100.0%	156	195	126	5	126					
7 SECGALEHGAWTLRPLCHLRCRCIFGAHLCLPLQTPRCDPKDFELASHAHGSPAGAPSLLL	100.0%	100.0%	156	195	180	5	180					
8 SECGALEHGAWTLRPLCHLRCRCIFGAHLCLPLQTPRCDPKDFELASHAHGSPAGAPSLLL	100.0%	100.0%	156	195	186	5	186					
9 LLPCMLLRLRPLDPAHPRSLVPVQLOERRPCCRPGIGHRL	100.0%	100.0%	156	195	223	5	223					
10 LLPCMLLRLRPLDPAHPRSLVPVQLOERRPCCRPGIGHRL	100.0%	100.0%	156	195	229	5	229					

**RESULT 7**  
 ABP6687 ID ABP66867 standard; protein; 229 AA.  
 XX AC ABP66887;  
 XX DT 09-DEC-2002 (first entry)  
 XX DR Human polyclonantide SEO ID NO 608.

XX Human; nootropic; neuroprotective; cyrostatic; dermatological; virucide; XX WPI; 2002-681727/73.  
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; DR DR N-ISDB; ABV83859.  
 KW anti-parkinsonian; antistickling; antianæmic; antiarthritic; cancer; XX PT Novel polypeptide useful for diagnosis, prognosis, prevention, and treatment of immune, hyperproliferative, renal, respiratory, PT cardiovascular, reproductive, endocrine, gastoointestinal and neurological disorders. PT PT PT PT  
 KW antihematic; hepatoprotective; cerebroprotective; antiinflammatory; PT  
 KW antiallergic; antidiabetic; antilulcer; anticonvulsant; antifungal; PT  
 KW antiparasitic; cariant; immune disorder; cardiovascular disorder; PT  
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine. PT  
 XX Homo sapiens.

OS XX SEQ ID NO 608; 369pp + Sequence Listing; English.

PN US20020390672-A1.

PD 11-JUL-2002.

XX PF 17-JAN-2001; 2001US-00764853.

XX PR 31-JAN-2000; 2000US-01793065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0222963P.  
 PR 26-JUL-2000; 2000US-022964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 22-AUG-2000; 2000US-0225758P.  
 PR 30-AUG-2000; 2000US-0226868P.  
 PR 01-SEP-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 05-SEP-2000; 2000US-0229355P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 08-SEP-2000; 2000US-0229513P.  
 PR 21-SEP-2000; 2000US-0231413P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 25-SEP-2000; 2000US-0234274P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-023935P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 01-NOV-2000; 2000US-0241809P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 08-DEC-2000; 2000US-025156P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 XX (ROSE/) ROSEN C. A.  
 PA (RUBE/) RUBEN S. M.  
 PA (BARA/) BARASH S. C.  
 XX Rosen CA, Ruben SM, Barash SC;

OS Homo sapiens.

PN US200190304-A2.

PD 29-NOV-2001.

XX	KW	chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
PP	KW	interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX	XX	
PR	OS	Unidentified.
XX	XX	
(HUMA-) HUMAN GENOME SCI INC.	PN	WO200286443-A2.
XX	XX	
PI	PD	31-OCT-2002.
XX	XX	
WPI: 2002-122018/16.	PF	18-APR-2002; 2002WO-US012476.
DR	XX	
N-PSDB; ABL90745.	PR	18-APR-2001; 2001US-0284770P.
XX	PR	10-MAY-2001; 2001US-0290494P.
PT	PR	09-NOV-2001; 2001US-0339245P.
PT	PR	13-NOV-2001; 2001US-035668P.
PT	PR	29-NOV-2001; 2001US-0334370P.
XX	PR	12-APR-2002; 2002US-0372246P.
PS	XX	
XX	PA	(EBSB-) EOS BIOTECHNOLOGY INC.
XX	XX	
The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABL89040-ABL89044) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <a href="http://ftp.wipo.int/pub/published-pct_sequences">FTP.wipo.int/pub/published-pct_sequences</a>		
Claim 11; SEQ ID NO 2712; 2081pp + Sequence Listing; English.	XX	
CC	XX	
CC	XX	The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient from a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
CC	XX	Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
CC	XX	Claim 27: Page 426; 453pp; English.
CC	XX	The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or pre-cancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hyper sensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated polypeptides of the invention.
CC	XX	Sequence 223 AA;
CC	XX	Query Match 83.9%; Score 187; DB 5; Length 223;
CC	XX	Best Local Similarity 100.0%; Pred. No. 1.3e-162;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	37	EVTKVATOKHRSQPLNTWSHFGTVTGSAGWGPBEPPLPSYRAFGEGASARPCCRCRNGT 96
Db	37	EVTKVATOKHRSQPLNTWSHFGTVTGSAGWGPBEPPLPSYRAFGEGASARPCCRCRNGT 96
Qy	97	CVLGSFCVCPAHTFGCYCHDQRSECGALEHGAWTLCRCLCIFGAHLCLPLOTPDR 156
Db	97	CVLGSFCVCPAHTFGCYCHDQRSECGALEHGAWTLCRCLCIFGAHLCLPLOTPDR 156
Qy	157	CDPKDFFLASHARGPAGGGAPSLLLPCMLLHRLRDPAPAHPRSLVPSVLQRRPGR 216
Db	157	CDPKDFFLASHARGPAGGGAPSLLLPCMLLHRLRDPAPAHPRSLVPSVLQRRPGR 216
Qy	217	PGLGHRL 223
Db	217	PGLGHRL 223
RESULT 9	Qy	97 CVLGSFCVCPAHTFGCYCHDQRSECGALEHGAWTLCRCLCIFGAHLCLPLOTPDR 156
ID ABU56711	Db	97 CVLGSFCVCPAHTFGCYCHDQRSECGALEHGAWTLCRCLCIFGAHLCLPLOTPDR 156
XX	Qy	37 EVTKVATOKHRSQPLNTWSHFGTVTGSAGWGPBEPPLPSYRAFGEGASARPCCRCRNGT 96
XX	Db	37 EVTKVATOKHRSQPLNTWSHFGTVTGSAGWGPBEPPLPSYRAFGEGASARPCCRCRNGT 96
DT 02-APR-2003 (first entry)	Qy	157 CDPKDFFLASHARGPAGGGAPSLLLPCMLLHRLRDPAPAHPRSLVPSVLQRRPGR 216
XX	Db	157 CDPKDFFLASHARGPAGGGAPSLLLPCMLLHRLRDPAPAHPRSLVPSVLQRRPGR 216
Lung cancer-associated polypeptide #3104.	Qy	217 PGLGHRL 223
XX	Qy	217 PGLGHRL 223
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;	Db	217 PGLGHRL 223
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;	Db	

**RESULT 10**  
 ADN39104 standard; protein; 223 AA.  
 XX  
 AC ADN39104;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:422.  
 XX  
 KW Human; differential expression; cancer; angiogenic disorder;  
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
 KW inflammatory disease; autoimmune disease;  
 KW retinal neovascularization syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiotonic; immunomodulatory;  
 KW pulmonary; gene therapy; vaccine.  
 OS Homo sapiens.  
 XX  
 PN WO2003042661-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 13-NOV-2002; 2002WO-US036810.  
 XX  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 21-NOV-2001; 2001US-0332464P.  
 PR 29-NOV-2001; 2001US-0334193P.  
 PR 03-DEC-2001; 2001US-0335394P.  
 PR 14-DEC-2001; 2001US-0340376P.  
 PR 08-JAN-2002; 2002US-0341211P.  
 PR 10-JAN-2002; 2002US-0341349P.  
 PR 08-FEB-2002; 2002US-0355250P.  
 PR 13-FEB-2002; 2002US-03556714P.  
 PR 20-FEB-2002; 2002US-03556714P.  
 PR 29-MAR-2002; 2002US-0359077P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-037246P.  
 PR 05-TUN-2002; 2002US-0388614P.  
 PR 16-JUL-2002; 2002US-0396839P.  
 PR 22-JUL-2002; 2002US-0397775P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezzi PA;  
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;  
 XX  
 DR WPI; 2003-468649/44.  
 XX  
 DR N-PSDB; ADN39103.  
 XX  
 PT Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosis or treating cancer, comprises detecting a nucleic acid in a biological sample.  
 XX  
 PS Claim 12; SEQ ID NO 422; 138pp; English.  
 XX  
 CC The invention relates to nucleic acids and proteins (ADN39683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and antibodies and methods are useful for diagnosing, prognosis and treating

CC cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularization syndrome, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.

CC sequence 223 AA;

CC

Query Match 83.9%; Score 187; DB 7; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-162;  
 Mismatches 0; Indels 0; Gaps 0;

XX

Qy 37 EVTKVATOKHRSQSPNWTSSHFGVNTGSABGWGPEPLPSRAFEGASAPRCCRNGGT 96  
 Db 37 EVTKVATOKHRSQSPNWTSSHFGVNTGSABGWGPEPLPSRAFEGASAPRCCRNGGT 96

Qy 97 CVLGSPFCVCPAHFTGRCEDQRSSECGALEHGAWTLRACHLCRCLFGALHCLPQTDR 156  
 Db 97 CVLGSPFCVCPAHFTGRCEDQRSSECGALEHGAWTLRACHLCRCLFGALHCLPQTDR 156

Qy 157 CDPKDFLASHAHGPAGAPSLLLPCALLHRLRPDAHPRSLVPSVLQRERRPGR 216  
 Db 157 CDPKDFLASHAHGPAGAPSLLLPCALLHRLRPDAHPRSLVPSVLQRERRPGR 216

Qy 217 PGLGRL 223  
 Db 217 PGLGRL 223

RESULT 11  
 ID ADN39975 standard; protein; 223 AA.  
 XX  
 ID ADN39975;  
 AC ADN39975;  
 AC ADN39975;  
 DT 17-JUN-2004 (first entry)  
 XX  
 DB Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C345.  
 XX  
 KW Human; differential expression; cancer; angiogenic disorder;  
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
 KW inflammatory disease; autoimmune disease;  
 KW retinal neovascularization syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiotonic; immunomodulatory;  
 KW pulmonary; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003042661-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 21-NOV-2001; 2001US-0332464P.  
 PR 29-NOV-2001; 2001US-0334193P.  
 PR 03-DEC-2001; 2001US-0335394P.  
 PR 14-DEC-2001; 2001US-0340376P.  
 PR 08-JAN-2002; 2002US-0341211P.  
 PR 10-JAN-2002; 2002US-0341349P.  
 PR 08-FEB-2002; 2002US-0355250P.  
 PR 13-FEB-2002; 2002US-03556714P.  
 PR 20-FEB-2002; 2002US-03556714P.  
 PR 29-MAR-2002; 2002US-0359077P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-037246P.  
 PR 05-TUN-2002; 2002US-0388614P.  
 PR 16-JUL-2002; 2002US-0396839P.  
 PR 22-JUL-2002; 2002US-0397775P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 XX  
 PR 05-JUN-2002; 2002US-035250P.  
 PR 13-FEB-2002; 2002US-0356714P.  
 PR 20-FEB-2002; 2002US-0359077P.  
 PR 29-MAR-2002; 2002US-036809P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-JUN-2002; 2002US-037246P.  
 PR 05-JUN-2002; 2002US-038614P.  
 PR 13-JUL-2002; 2002US-039775P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX PD 31-MAR-2005.  
 XX XX  
 PI Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;  
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;  
 XX PR 14-SEP-2004; 2004WO-US029967.  
 DR 15-SEP-2003; 2003US-0503046P.  
 DR (RERE-) RES DEV FOUND.  
 XX PA  
 XX PI Vale W, Gray PC, Harrison CA;  
 PT Vale W, Gray PC, Harrison CA;  
 PT DR 2005-242562/25.  
 PT Augmenting signaling of a ligand of receptor serine kinase in a cell  
 PT comprises inhibiting the formation of complexes between Cripto and the  
 PT ligand on the surface of the cell.  
 XX  
 PS Disclosure; SEQ ID NO 4; 60pp; English.  
 PS XX  
 CC This invention relates to a novel method for augmenting signaling of a  
 CC ligand of a receptor serine kinase within a cell by inhibiting the  
 CC formation of complexes between Cripto and this ligand on the surface  
 CC of the cell. Specifically, it refers to TGF-beta and activin which are the  
 CC ligands of serine kinase receptors and which regulate tissue homeostasis  
 CC by activating the Smad2/3 intracellular signaling pathway, disruption of  
 CC this signaling pathway is associated with oncogenesis and tumorigenesis.  
 CC As such, the present invention describes a method for augmenting Smad2/3  
 CC signaling in a cell by administering a mutant ligand that retains  
 CC signaling activity but is unable to bind to Cripto, and thus bypasses  
 CC antagonism by Cripto. Note that augmentation of signaling increases  
 CC phosphorylation and activation of Smad2 and Smad3 in the cell, such that  
 CC it decreases the proliferative rate of the cell. The receptor serine  
 CC kinase is a type I activin receptor-like kinase-4 or -5 (ALK-4 or ALK-5)  
 CC and the formation of complexes is inhibited by suppressing expression of  
 CC Cripto using antisense oligonucleotides (siRNA) directed against Cripto,  
 CC and also mutating at least one allele of Cripto by homologous  
 CC recombination. Accordingly, pharmaceutical compositions derived thereof  
 CC exhibit cytostatic activity. This polypeptide sequence is the human  
 CC Criptic protein, a member of the EGF-CFC (Epidermal Growth Factor-Cripto,  
 CC FPL-1, Criptic) family of proteins of the invention.  
 XX Sequence 223 AA;  
 SQ Sequence 223 AA;  
 Query Match 83.9%; Score 187; DB 7; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-162;  
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 37 EVTRVATQHRSQPLNWTSFHFGTVTGSSEGWBPEPLYSRAFEGASARPRCCRNGT 96  
 Db 37 EVTRVATQHRSQPLNWTSFHFGTVTGSSEGWBPEPLYSRAFEGASARPRCCRNGT 96  
 Qy 37 EVTRVATQHRSQPLNWTSFHFGTVTGSSEGWBPEPLYSRAFEGASARPRCCRNGT 96  
 Db 97 CVLGSEFCVCPAHTFGRYCHDQRRESECGALEHGAWTLRACHLRCIFGAHLHCLPQTPDR 156  
 Qy 97 CVLGSEFCVCPAHTFGRYCHDQRRESECGALEHGAWTLRACHLRCIFGAHLHCLPQTPDR 156  
 Db 97 CVLGSEFCVCPAHTFGRYCHDQRRESECGALEHGAWTLRACHLRCIFGAHLHCLPQTPDR 156  
 Qy 157 CDPKDFLASHAHPGSSAGAPSLLLPCMLLHRLPDPAPRSLVPSVQLQERRPGCR 216  
 Db 157 CDPKDFLASHAHPGSSAGAPSLLLPCMLLHRLPDPAPRSLVPSVQLQERRPGCR 216  
 Qy 217 PGLGHRL 223  
 Db 217 PGLGHRL 223  
 Qy 157 CDPKDFLASHAHPGSSAGAPSLLLPCMLLHRLPDPAPRSLVPSVQLQERRPGCR 216  
 Db 157 CDPKDFLASHAHPGSSAGAPSLLLPCMLLHRLPDPAPRSLVPSVQLQERRPGCR 216  
 RESULT 12  
 ADY85963 ID ADY85963 standard; protein; 223 AA.  
 XX  
 AC ADY85963;  
 XX DT 16-JUN-2005 (first entry)  
 XX DE Human Criptic protein, a member of the EGF-CFC family Seq 4.  
 XX KW cell signaling; oncogenesis; antisense therapy; cytostatic; mutagenesis;  
 KW protein interaction; oncoprotein.  
 XX OS Homo sapiens.  
 XX PN WO2005028433-A2.  
 XX

RESULT 13  
 AAU16957 ID AAU16957 standard; protein; 231 AA.  
 XX AC AAU16957;  
 XX DT 07-NOV-2001 (first entry)  
 XX DE Human novel secreted protein, SEQ ID 198.

KW Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;  
 KW cardiotonic; vasotonic; cerebroprotective; nootropic; neuroprotective;  
 KW anti bacterial; virucide; fungicide; Ophthalmological; vulnerary;  
 KW secreted protein; rheumatoïd arthritis; hyperproliferative disorder;  
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;  
 KW cerebral ischaemia; angiogenesis; nervous system disorder;  
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
 KW wound healing; epithelial cell proliferation; skin ageing; food additive;  
 KW preservative; antiproliferative;  
 XX Homo sapiens.  
 XX WO200155141-A2.  
 PD 02-AUG-2001.  
 XX 02-AUG-2001; 2001WO-US001320.  
 PF 17-JAN-2001; 2000US-0179065P.  
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 PR 30-AUG-2000; 2000US-0225759P.  
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 PR 01-SEP-2000; 2000US-0229344P.  
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 PR 08-NOV-2000; 2000US-024524P.  
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 PR 08-NOV-2000; 2000US-024527P.  
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 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.

PR 06-DBC-2000; 2000US-0251479P.	XX	16-APR-1997	(first entry)
PR 08-DBC-2000; 2000US-0251856P.	DT		
PR 08-DBC-2000; 2000US-0251868P.	XX		Human criptin growth factor.
PR 08-DBC-2000; 2000US-0251869P.	XX		Criptin growth factor; CGF; angiogenesis; wound healing; vulnerability; muscle wastage; osteoporosis; implant fixation; tissue regeneration; pancreas cancer; diagnosis; gene therapy.
PR 08-DEC-2000; 2000US-0251989P.	XX		
PR 11-DBC-2000; 2000US-0251909P.	XX		
PR 11-JAN-2001; 2001US-0259678P.	XX		
PA (HUMA-) HUMAN GENOME SCI INC.	OS		
XX Homo sapiens.	XX		
PI Barash SC, Ruben SM;	Key		Location/Qualifiers
XX	PH	1.	
DR WPI-2001-476222/51.	Peptide	.23	
XX	FT	/label=	Sig_peptide
DR N-PSDB; AAS2862.	XX		
XX	PN	W09639420-A1.	
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to	XX		
PT diagnose diseases or disorders associated with aberrant expression or	XX		
PT activity of polypeptides, for treating blood clotting disorder,	XX		
PT hemophilia.	XX		
PS Claim 11; SEQ ID NO 198; 601pp; English.	XX	05-JUN-1995;	95WO-US007087.
XX	XX		
CC The invention relates to isolated nucleic acid molecules and their	PA		
CC encoded secreted proteins. The nucleic acids and proteins are used to	(HUMA-) HUMAN GENOME SCI INC.		
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,	XX		
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used	PI		
CC in diagnosing a pathological condition or susceptibility to a	XX		
CC pathological condition. Antibodies to the proteins can also be used in	XX		
CC alleviating symptoms associated with the disorders and in diagnostic	DR		
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays	WPI; 1997-043055/04.		
CC (ELISA). Disorders which are diagnosed or treated include autoimmune	N-PSDB; AAT51058.		
CC diseases e.g. rheumatoid arthritis, hyperpliative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac	XX		
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,	XX		
CC nervous system disorders e.g. Alzheimer's disease, infections caused by	CC		Human criptin growth factor (CGF) (AAW09111) is a novel polypeptide
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,	CC		structurally related to human criptin growth factor. It is overexpressed
CC and many other disorders listed in the specification. The polypeptides	CC		and secreted by certain types of cancer cells e.g. pancreatic cancers.
CC can also be used to aid wound healing and epithelial cell proliferation,	CC		Recombinant CGF can be produced in host cells utilising vectors
CC to prevent skin aging due to sunburn, to maintain organs before	CC		incorporating a CGF cDNA clone (AAW51058) isolated from a human
CC transplantation, for supporting cell culture of primary tissues, to	CC		pancreatic cancer tissue cDNA library. CGF can be used to treat e.g.
CC regenerate tissues in chemotaxis. The polypeptides can also be used	CC		muscle wasting diseases, osteoporosis, to aid implant fixation, to
CC as a food additive or preservative to increase or decrease storage	CC		stimulate tissue regeneration and wound healing, to promote angiogenesis
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,	CC		and to stimulate proliferation of vascular smooth muscle and endothelial
CC minerals, cofactors and other nutritional components. The present	CC		cell prodrn. It can also be used as a marker for cancer diagnosis
CC sequence represents a novel secreted protein of the invention. Note: The	XX		
CC	Sequence 230 AA;		
Query Match 83.9%; Score 197; DB 4; Length 231;			
Best Local Similarity 100.0%; Pred. No. 1.3e-162;		66.8%;	Score 149; DB 2;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Length 230;	Length 230;
Qy 37 EVTRVATQHRSPLNWTSHFGEVTSAGWGPBPEPLYSRAFGEGASARPCCRNGT	Qy	Best Local Similarity 100.0%; Pred. No. 8.1e-128;	
Db 45 EVTRVATQHRSPLNWTSHFGEVTSAGWGPBPEPLYSRAFGEGASARPCCRNGT	Db	Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 97 CVLGSEFCVCPAHTFGRYCHDQRRECGALEHGAWTLRACHLCRCIFGAHLHCLPLQTPDR	Qy	37 EVTRVATQHRSPLNWTSHFGEVTSAGWGPBPEPLYSRAFGEGASARPCCRNGT	96
Db 105 CVLGSEFCVCPAHTFGRYCHDQRRECGALEHGAWTLRACHLCRCIFGAHLHCLPLQTPDR	Db	97 CVLGSEFCVCPAHTFGRYCEHDQRRECGALEHGAWTLRACHLCRCIFGAHLHCLPLQTPDR	164
Qy 157 CDPKDFFLASHAHGPGSAGGAPSLLLPCALIHLRLPDAHPRSLVPSVLQERRPGCR	Qy	97 CVLGSEFCVCPAHTFGRYCEHDQRRECGALEHGAWTLRACHLCRCIFGAHLHCLPLQTPDR	156
Db 165 CDPKDFFLASHAHGPGSAGGAPSLLLPCALIHLRLPDAHPRSLVPSVLQERRPGCR	Db	157 CDPKDFFLASHAHGPGSAGGAPSLLLPCALIHLRLPDAHPRSLVPSVLQERRPGCR	224
Qy 217 PGLGHL 223	Qy	157 CDPKDFFLASHAHGPGSAGGAPSLLLPCALIHLRLPDAHPRSLVPSVLQERRPGCR	185
Db 225 PGLGHL 231	Db	157 CDPKDFFLASHAHGPGSAGGAPSLLLPCALIHLRLPDAHPRSLVPSVLQERRPGCR	185
RESULT 15			
ID AAC77914			
ID AAC77914 standard; protein: 223 AA.			
XX XX			
AC AC			
AC AAC77914;			
XX XX			
AC AAC77914;			
DT DT			
23-JAN-2002 (first entry)			
AAW09111;			

XX Human cryptic-like polypeptide.  
 XX  
 KW Cryptic; human; cytosstatic; cardiant; nootropic; neuroleptic; cancer;  
 KW antiasthmatic; anti-angiogenic; gene therapy; lung cancer; asthma;  
 KW respiratory disease; epilepsy; schizophrenia; depression; hyperactivity;  
 KW heart hypertrophy; heart failure; cardiomyopathy; angiogenesis;  
 KW vasculogenesis.  
 XX

OS Homo sapiens.

XX PN WO20017322-A1.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-EP003965.

XX DR N-PSDB; AAH77168.

XX PR 10-APR-2000; 2000EP-00107142.

XX PA (MERE ) MERCK PATENT GMBH.

XX PI Duecker K;

XX XX WPI; 2002-017462/02.

XX DR AAH77168.

XX PT Novel cryptic-like secreted polypeptide found in various tumors and

PT organs is useful to treat diseases including cancer, particularly lung

PT cancer, asthma and heart disease.

XX

PS Claim 1; Page 33-34; 37pp; English.

XX

CC The sequence represents the novel human cryptic-like secreted protein of  
 CC the invention. The polypeptide of the invention has cytosstatic, cardiant,  
 CC nootropic, neuroleptic, antiasthmatic, and anti-angiogenic activity, and  
 CC has a use in gene therapy. The polypeptide and polynucleotide of the  
 CC invention may be used to treat cancer, particularly lung cancer,  
 CC respiratory diseases, asthma, epilepsy, schizophrenia, depression,  
 CC hyperactivity, heart hypertrophy, heart failure, cardiomyopathies,  
 CC aberrant angiogenesis and vasculogenesis.

XX Sequence 223 AA;

Qy 79 AFGEGASARPRCCRNGGTCVGSFRCVCPAHTGRCYCEHDDORSEGALEHGAWTLRACHL 138  
 Db 79 AFGEGASARPRCCRNGGTCVGSFRCVCPAHTGRCYCEHDDORSEGALEHGAWTLRACHL 138  
 Qy 139 CRCIFGALHCLPLQTPDRCDPKDPLASHAHAHGSAGGAPSILLIPCALHRLRDPDAPH 198  
 Db 139 CRCIFGALHCLPLQTPDRCDPKDPLASHAHAHGSAGGAPSILLIPCALHRLRDPDAPH 198  
 Qy 199 PRSLVPSVLOERRPGPGLGHLR 223  
 Db 199 PRSLVPSVLOERRPGPGLGHLR 223

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RL Nature 434:724-731 (2005).  
 RN [3] NUCBOTIDS SEQUENCE [LARGE SCALE MRNA].  
 RP TISSUE=lung;  
 RC MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Kleuser R.L., Peingold A.A., Grouse L.H., Degeje J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleth F.,  
 RA Diatchenko L., Matsuska K., Farmer A.P., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rata S.S., Loquelleau N.A., Peters G.J., Abramson R.D., Mullally S.J.,  
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Murry D.M., Soderoren B.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Heitton R., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M., Smalius D.E.,  
 RA Schneir A., Schein J.B., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4] VARIANT TRP-78, AND INVOLVEMENT IN DTGA AND CTRM.  
 RX PubMed=11799476;  
 RA Goldmuntz B., Bamford R., Karkera J.D., dela Cruz J., Roessler E.,  
 RA Muenke M.;  
 RT "CFC1 mutations in patients with transposition of the great arteries  
 and double-outlet right ventricle";  
 RT Am. J. Hum. Genet. 70:776-780 (2002).  
 CC -I- FUNCTION: Involved in the correct establishment of the left-right  
 axis. May play a role in mesoderm and/or neural patterning during  
 gastrulation.  
 CC -I- PTM: N-glycosylated (By similarity).  
 CC -I- Defects in CFC1 are a cause of visceral heterotaxy (HTX)  
 [MM:605376]. HTX is an autosomal form of visceral heterotaxy  
 (HTX). HTX is characterized by a variable group of congenital  
 anomalies that include complex cardiac malformations and situs  
 inversus or situs ambiguus.  
 CC -I- DISBASE: Defects in CFC1 are a cause of transposition of the great  
 arteries, dextro-looped (DTGA) [MM:608808]. The more common form  
 of DTGA, consists of complete inversion of the great vessels, so  
 that the aorta incorrectly arises from the right ventricle and the  
 pulmonary artery incorrectly arises from the left ventricle. This is  
 an arrangement that is incompatible with life. Patients  
 with this arrangement have atrial and/or ventricular septal defects or other types  
 of shunting that allow some mixing between the circulations in  
 order to support life minimally, but surgical intervention is  
 always required.  
 CC -I- DISBASE: Defects in CFC1 are a cause of conotruncal heart  
 malformations (CTRM) [MM:217095]. CTRM consist of cardiac outflow  
 tract defects, such as tetralogy of Fallot, pulmonary atresia,  
 double-outlet right ventricle, truncus arteriosus communis, and  
 aortic arch anomalies.  
 CC -I- SIMILARITY: Contains 1 EGF-like domain.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC  
 DR EMBL; AR312769; ARG30294.1; mRNA.  
 DR EMBL; AR312925; ARG42475.1; Genomic DNA.  
 DR EMBL; AC013269; ARY1495.1; Genomic DNA.  
 DR EMBL; BC069508; AAH69508.1; mRNA.  
 DR EMBL; BC074825; ARH74825.1; mRNA.  
 DR EMBL; BC074826; ARH74826.1; mRNA.  
 DR EMBL; BC110080; ARH10081.1; mRNA.  
 DR MEDLINE; P07850; ITPC.  
 DR Hsnc; HGNC:18292; CFC1.  
 DR NIM; 217095; phenotype.  
 DR NIM; 605194; gene.  
 DR NIM; 605376; phenotype.  
 DR NIM; 605376; phenotype.  
 DR GO; GO:0007368; P: determination of left/right symmetry; NAS.  
 DR InterPro; IPR00742; EGF\_3.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR013032; EGF-like\_reg.  
 DR PF00008; EGF\_1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS00026; EGF\_3; 1.  
 KW Gastrolulation; Glycoprotein; Disease mutation; EGF-like domain;  
 KW Glycoprotein; Signal.  
 FT SIGNAL; 1 25  
 FT CHAIN; 26 223  
 FT CRYPTIC PROTEIN.  
 /FTID=PRO\_0000044630.  
 FT EGF-like.  
 FT N-linked (GLCNAC. . .) (Potential).  
 FT DOMAIN; 86 115  
 FT CARBOHYD; 52 52  
 FT DISULFID; 90 97  
 FT DISULFID; 91 103  
 FT DISULFID; 105 114  
 FT VARIANT; 78 78  
 FT VARIANT; 112 112  
 FT VARIANT; 126 126  
 FT R > W (in dbsNP: 2579433).  
 /FTID=VAR\_024322.  
 FT C (in HTMX; complete loss of  
 activity; abnormal cell surface  
 localization).  
 /FTID=VAR\_034323.  
 FT R > C.  
 /FTID=VAR\_024324.  
 SQ SEQUENCE; 223 AA; 24612 MW; B52852A00ABC1A3 CRC64;  
 Query Match 83.9%; Score 187; DB 1; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-172; 0; Gaps 0;  
 Matches 187; Conservative 0; Mismatches 0;  
 QY 37 EYTTKAVQKHSQSPNNTSSHEGVTSAAEGKGPPEEPYPSRAFGEGASARPRCCRNGT 96  
 DB 37 EYTTKAVQKHSQSPNNTSSHEGVTSAAEGKGPPEEPYPSRAFGEGASARPRCCRNGT 96  
 QY 97 CTVLGSFCVCPAHTGTYCEHDORSSCAEGAWTACHLCRIGALHCLPLQTPDR 156  
 DB 97 CTVLGSFCVCPAHTGTYCEHDORSSCAEGAWTACHLCRIGALHCLPLQTPDR 156  
 QY 157 CDPKDFLASHAHPGSAAGAPSLLLPCALHLRDAPIPLVPSVLRERPGCR 216  
 DB 157 CDPKDFLASHAHPGSAAGAPSLLLPCALHLRDAPIPLVPSVLRERPGCR 216  
 QY 217 PGIGHRL 223  
 DB 217 PGIGHRL 223  
 RESULT 2  
 CFC1\_MOUSE STANDARD; PRT; 202 AA.  
 ID CFC1\_MOUSE STANDARD;  
 AC P97766; Q49605; Q9J1B7;  
 DT 20-DEC-2005; integrated into UniProtKB/Swiss-Prot.  
 DT 01-MAY-1997; sequence version 1.  
 DT 07-MAR-2006; entry version 30.  
 DE Cryptic protein precursor.  
 Name=Cfc1;  
 GN Mus musculus (Mouse);  
 OC BukaYvota; Merakoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Butharia; Buarchontoglires; Gires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, TISSUE SPECIFICITY,  
 DE DEVELOPMENTAL STAGE, AND GLYCOSYLATION.  
 OS STRAIN=129/SV;  
 RC MEDLINE; P07850; ITPC.  
 RX Wang M.M., Leder P.;  
 RA Shen M.M., Wang H.; Leder P.;  
 RT "A differential display strategy identifies Cryptic, a novel EGF-

related gene expressed in the axial and lateral mesoderm during mouse gastrulation."; Development 124: 429-442 (1997).

[2] NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA]. MEDLINE=22388257; PubMed=12477332; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F., Wagner L., Shemesh C.M., Schulier G.D., Altenschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Hara S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[3] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-154. MEDLINE=20490697; PubMed=11024280; DOI=10.1016/S0378-1119(00)00337-1; Colas J.-F., Schoenwolf G.C.; "Subtractive hybridization identifies chick-cripto, a novel BGF-CFC ortholog expressed during gastrulation, neurulation and early

cardiogenesis.";

[4] Gene 255:205-217 (2000).

PP FUNCTION, AND KNOCK-OUT. MEDLINE=20045034; PubMed=10574770; DOI=10.1016/S0960-9822(00)80059-7;

GAIO U., SCHWEICKERT A., FISCHER A., GARRETT A.N., MUELLER T., GEZELLA C., LANKES W., STREHLE M., BRITSCH S., BLUM M., BIRCHMEIER C.

"A role of the cryptic gene in the correct establishment of the left-right axis";

Cur. Biol. 9:1339-1342 (1999).

-1- FUNCTION: Involved in the correct establishment of the left-right axis. May play a role in mesoderm and/or neural patterning during gastrulation.

-1- TISSUE SPECIFICITY: No expressed in adult tissues.

-1- DEVELOPMENTAL STAGE: Expressed during Gastrulation (from 6.5 dpc to 11 dpc) in two spatial domains that correspond to the axial and lateral mesoderm. In the first domain expression is progressively localized to the anterior primitive streak, the head process, and the node and notochordal. In the second domain, expression is initially concentrated in the lateral region of the egg cylinder, and is later found circumferentially in the intermediate and lateral plate mesoderm. Furthermore, the expression can also be detected at the early head-fold stage in the midline neuroectoderm, and consequently is an early marker for the prospective floor plate of the neural tube. Expression ceases at the end of gastrulation, and has not been observed in later embryonic stages.

-1- PTM: N-glycosylated.

-1- MISCELLANEOUS: Mice lacking functional Cfc1 showed positional defects in internal organs. The lung presents a right pulmonary isomerism. The stomach is located on either the left or the right and the spleen is small and has an abnormal shape. The apex of the heart pointed to the right or left. In addition malpositioning of heart outflow tracts is observed, the aorta is connected to the right ventricle and emerged from the heart in a ventral position and to the right of the pulmonary artery. This one is connected to either the left or the right ventricle.

-1- SIMILARITY: Contains 1 EGF-like domain.

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EMBL; U57270; AAC533042_1; -; mRNA.					
EMBL; BC100705; AAII0706_1; -; mRNA.					
EMBL; BC100706; AAII0707_1; -; mRNA.					
EMBL; BC100708; AAII0709_1; -; mRNA.					
EMBL; BC100711; AAII0712_1; -; mRNA.					
EMBL; AF242430; AAFT6323_1; -; Genomic_DNA.					
HSSP; P00749; 1URK					
Ensembl; ENSMUSG00000026124; <i>Mus musculus</i> .					
MGI; MGI:109448; Cfcl.					
GO; GO:0005615; C:extracellular space; TAS.					
InterPro; IPR000742; EGF_3.					
InterPro; IPR006220; EGF_like.					
InterPro; IPR012032; EGF_like_reg.					
Ptarm; PF000008; EGF_1.					
PROSITE; PS00022; EGF_1; 1.					
PROSITE; PS01186; EGF_2; FALSE_NEG.					
PROSITE; PS05022; EGF_3; 1.					
Developmental_protein; EGF-like_domain; Gastrulation; Glycoprotein; Signal.	1	35	Potential.		
CHAIN	36	202	Cryptic_protein.		
			/PTID=PRO_0000044631.		
DOMAIN	94	123	EGF-like.		
CARBOHYD	65	65	N-linked (GlcNAc. . .) (Potential).		
DISULFID	98	105	By similarity.		
DISULFID	99	111	By similarity.		
DISULFID	113	122	By similarity.		
DISULFID	83	83	P > T (In Ref. 2; AAI00707).		
CONFLICT			570355AD339A16FD7 CRC64;		
SEQUENCE	202 AA	21792 MW			

```

S U R S U L T 3
U2296 XENLA  PRELIMINARY; PRT; 191 AA.
Q2UZ96; 24-JAN-2006; integrated into UniProtKB/TREMBL.
24-JAN-2006; sequence version 1.
07-FEB-2006; entry version 2.
Crypto-2.
Name=CR2;
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopidae; Xenopus; Xenopus.
NCBI_TaxID=8355;
[1]
[1]
NUCLEOTIDE SEQUENCE.
DOREY K.; HILL C.S.; "Role of BGF-CFC family members in Nodal signalling during early
Xenopus development"; Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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EMBL; AJ861899; CAI15753.1; -; mRNA.
SEQUENCE 191 AA; 21651 MW; D4E992122C89495D CRC64;
SEQUENCE 191 AA; 6.34; Score 14; DB 2; Length 191;
Query Match 6.1%; Score 15; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
93 NGGTCVLGSCFCVCPA 107
[1]
[1]
101 NGGTCVLGSCFCVCPA 115

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EMBL; U57720; AAC534042; 1; mRNA.					
EMBL; BC100705; AA100706; 1; mRNA.					
EMBL; BC100706; AA100707; 1; mRNA.					
EMBL; BC100708; AA100708; 1; mRNA.					
EMBL; BC100711; AA100709; 1; mRNA.					
EMBL; AF242430; AF242430; 1; Genomic_DNA.					
HSSP; P00749; 1URK					
Ensembl; ENSMUSG0000026124; <i>Mus musculus</i> .					
MGI; MGI:109448; CEC1.					
GO; GO:0005615; C: extracellular space; TAS.					
Intero; IPR000742; EGF_3.					
Intero; IPR0062209; EGF-like.					
Intero; IPR013032; EGF-like_reg.					
Pfam; PF00008; EGF_1.					
PROSITE; PS00022; EGF_1.					
PROSITE; PS01186; EGF_2.					
PROSITE; PS00028; EGF_3.					
Developmental protein; EGF-like domain; Gastrulation; Glycoprotein; Signal.					
SIGNAL_CHAIN	1	35	Potential.		
SIGNAL_CHAIN	36	202	Cryptic protein.		
DOMAIN	94	123	/PTId=PRO_000044631.		
CARBONYL	65	65	EGF-like.		
DISULFID	98	105	N-linked (GlcNAc . . .) (Potential).		
DISULFID	99	111	By Similarity.		
DISULFID	113	122	By Similarity.		
CONFLICT	83	83	P → T (In ref. 2; AA100707).		
SEQUENCE	202 AA;	21792 MW;	57025 AD3359A16FD7 CRC64;		



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CC EMBL; AX796189; AX81599.1; - ; mRNA.  
KW EGFP-like domain; Repeat  
SQ 251 AA; 27849 MN; D0DFCC140A3E0BFE CRC64;

Query Match 4.9%; Score 11; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 0.083; 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 93 NGGTCVGLGSPC 103  
Db 152 NGGTCVGLGSPC 162

RESULT 8  
Q53M57\_ORYSA PRELIMINARY; PRT; 105 AA.

ID Q53M57\_ORYSA  
AC Q53M57;  
DT 24-MAY-2005, integrated into UniProtKB/TREMBL.  
DT 07-FEB-2006, entry version 3.

DE Expressed protein.  
ORName=LOC\_Os01g14190;  
OS *Oryza sativa* (Japonica cultivar-group); Embryophyta; Tracheophyta;  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poaceae; BEP Clade;  
NCBI\_TaxID=39947;

RN [1]  
NUCLEOTIDE SEQUENCE.  
Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,

RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblyum T., Taitrin T.,  
RA Bera J., Kim M., Jin S., Farrosh H., Vuong H., Overton II L.,  
RA Reardon M., Weaver B., Johri S., Lewis M., Utterback T., Van Aken S.,  
RA Wortman J., Haas B., Koo H., Zismann V., Hsiao J., Lobst S.,  
RA de Vazeilles A., White O., Salzberg S., Fraser C.,  
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
RL [2]  
NUCLEOTIDE SEQUENCE.  
RA Buell R.; Wing R.A.; McCombie W.A.; Ouyang S.;  
RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
RL [3]  
NUCLEOTIDE SEQUENCE.  
RA Buell C.R.; Wing R.A.; McCombie W.A.; Ouyang S.;  
RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
RL [4]  
NUCLEOTIDE SEQUENCE.  
RA Buell C.R., Wing R.A., McCombie W.A., Ouyang S.;  
RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AC137924; AX96767.1; - ; Genomic DNA.  
DR EMBL; DPO00010; ARA92348.1; - ; Genomic DNA.  
SQ SEQUENCE 105 AA; 11604 MN; 91390CAG01836B7C CRC64;

Query Match 3.6%; Score 8; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 0.32; 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSLLLLP 183  
Db 73 PSLLLLP 80

RESULT 9  
Q6DB65\_ORYSA PRELIMINARY; PRT; 105 AA.

ID Q6DB65\_ORYSA  
AC Q6DB65;  
DT 23-NOV-2004, integrated into UniProtKB/TREMBL.  
DT 23-NOV-2004, sequence version 1.  
DT 07-FEB-2006, entry version 6.  
DE Hypothetical protein OSJNBA0073E05.11.  
GN Name=OSJNBA0073E05.11;

OS *Oryza sativa* (japonica cultivar-group); Embryophyta; Tracheophyta;  
OC Viridiplantae; Streptophyta; Embryophyta; Liliopsida; Poaceae; BEP Clade;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP Clade;  
OC Bihartooideae; Oryzeae; Oryza.  
NCBI\_TaxID=39947;

RN [1]  
NUCLEOTIDE SEQUENCE.  
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,  
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,  
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,  
RA Hsiau J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,  
RA Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,  
RA Wu H.-P., Shaw J.-F.,

RT "Oryza sativa BAC OSJNBA0073E05 genomic sequence.";  
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

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CC DR EMBL; AC136219; AAV31337.1; - ; Genomic DNA.

DR Gramene; Q60565; -

KW Hypothetical protein.

SQ SEQUENCE 105 AA; 10289 MW; 48F3E18C287B182 CRC64;

Qy 176 PSLLLLP 183  
Db 42 PSLLLLP 49

CC Query Match 3.6%; Score 8; DB 2; Length 105;  
CC Best Local Similarity 100.0%; Pred. No. 32; 0;  
CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 186 LLHRLRP 193  
Db 102 LLHRLRP 109





DR GO; GO:0015428; P:type I protein secretor activity; IEA.  
DR GO; GO:0009306; P:protein secretion; IEA.  
DR InterPro; IPR006143; Hyd.  
DR InterPro; IPR003997; RxnD\_bac.  
DR PRINTS; PRO1490; RXNTOXIND.  
DR TIGRFAMS; TIGR01730; RND\_mfp; 1.  
KW Signal.  
FT SIGNAL 1 28 Potential.  
SQ SEQUENCE 357 AA; 39181 MW; BBB91CA932116A3 CRC64;  
Query Match 3.6%; Score 8; DB 2; Length 357;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 180 LLFCALL 187  
| | | | | | | |  
Db 11 LLFCALL 18

Search completed: September 22, 2006, 19:00:17  
Job time : 302 secs

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OM protein - protein search, using SW model

Run on: September 22, 2006, 19:00:34 ; Search time 49 Seconds (without alignments)

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTWRRHVRLLFTVSIAQII.....PSVLRERRRPCGRPGIGHRL 223

Scoring table: OLIGO Gapext 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1685

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

1: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/5\_COMB.pep:\*

2: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/6\_COMB.pep:\*

3: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/7\_COMB.pep:\*

4: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/8\_COMB.pep:\*

5: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/9\_PCTUS\_COMB.pep:\*

6: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/10\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3\_ptodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	149	66.8	230	1 US-08-471-371-2	Sequence 2, Appli
2	8	3.6	363	2 US-09-252-991A-18016	Sequence 18016, A
3	8	3.6	2523	1 US-08-432-18	Sequence 432-18
4	8	3.6	2523	2 US-08-899-232-3	Sequence 3, Appli
5	8	3.6	2523	2 US-09-121-457-3	Sequence 3, Appli
6	7	3.1	69	9115	Sequence 9115, Ap
7	7	3.1	70	2 US-09-621-976-3356	Sequence 5356, Ap
8	7	3.1	88	2 US-09-61-97-393	Sequence 3988, Ap
9	7	3.1	103	2 US-09-621-976-515	Sequence 5415, Ap
10	7	3.1	106	2 US-09-149-476-341	Sequence 341, Ap
11	7	3.1	107	2 US-09-461-325-484	Sequence 484, App
12	7	3.1	107	2 US-10-012-542-184	Sequence 484, App
13	7	3.1	107	2 US-10-115-123-184	Sequence 484, App
14	7	3.1	111	2 US-09-248-796A-26807	Sequence 26807, A
15	7	3.1	112	2 US-09-621-976-3926	Sequence 3926, Ap
16	7	3.1	115	2 US-10-104-047-1840	Sequence 3840, Ap
17	7	3.1	119	2 US-09-991-181-165	Sequence 165, App
18	7	3.1	119	2 US-09-444-165	Sequence 165, App
19	7	3.1	119	2 US-09-997-333-165	Sequence 165, App
20	7	3.1	119	2 US-09-992-598-165	Sequence 165, App
21	7	3.1	119	2 US-09-989-735-165	Sequence 165, App
22	7	3.1	119	3 US-09-989-726-165	Sequence 165, App
23	7	3.1	119	3 US-09-997-514-165	Sequence 165, App
24	7	3.1	119	3 US-09-989-728-165	Sequence 165, App
25	7	3.1	119	3 US-09-997-349-165	Sequence 165, App
26	7	3.1	119	3 US-09-997-653-165	Sequence 165, App

## ALIGNMENTS

RESULT 1  
US-08-471-371-2  
; Sequence 2, Application US/08471371  
; Patent No. 5981215  
; GENERAL INFORMATION:  
; APPLICANT: Meissner, Paul S.  
; APPLICANT: Coleman, Timothy A.  
; TITLE OF INVENTION: HUMAN CRIPTIN GROWTH FACTOR  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
; STREET: STEWART & OLSTEIN  
; CITY: 6 Becker Farm Road  
; STATE: Rose, and  
; COUNTRY: U.S.A.  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,371  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferraro, Gregory D.  
; REGISTRATION NUMBER: 36-134  
; REFERENCE/DOCKET NUMBER: 322580-455  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (201) 994-1700  
; TELEFAX: (201) 994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 230 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-471-371-2

Query Match 66.8%; Score 149; DB 1; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.7e-136;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 EIVTKVATQKHSQPLNWTSFHGEVTSAGNGPPEPLPYSRAFGEGASARPRCCNGGT 96  
Db 37 EIVTKVATQKHSQPLNWTSFHGEVTSAGNGPPEPLPYSRAFGEGASARPRCCNGGT 96

Qy 97 CVLGSFCVCPAHTGRCYCIDQRSSCGALEHGANTLRACHLRCIFGALHCLPLQTPDR 156  
 ; Sequence 18016, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSUEDOMONAS  
 ; FILE REFERENCE: 10719.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 18016  
 ; LENGTH: 363  
 ; TYPE: PRT  
 ; ORGANISM: *Psuedomonas aeruginosa*  
 US-09-252-991A-18016

Query Match 3.6%; Score 8; DB 2; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 8; Conservative 0; Mismatches 0;  
 Gaps 0;  
 Indels 0;

Qy 157 CDPKDFLASHAGPSAGGAPLLLPCPA 185  
 Db 157 CDPKDFLASHAGPSAGGAPLLLPCPA 185

RESULT 2  
 US-09-252-991A-18016  
 ; Sequence 18016, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSUEDOMONAS  
 ; FILE REFERENCE: 10719.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 18016  
 ; LENGTH: 363  
 ; TYPE: PRT  
 ; ORGANISM: *Psuedomonas aeruginosa*  
 US-09-252-991A-18016

Query Match 3.6%; Score 8; DB 2; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 8; Conservative 0; Mismatches 0;  
 Gaps 0;  
 Indels 0;

Qy 91 CRNGGTCV 98  
 Db 265 CRNGGTCV 272

RESULT 4  
 US-08-899-232-3  
 ; Sequence 3, Application US/08899232  
 ; Patent No. 6436650  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Artavanis-Tsakonas, Spyridon  
 ; FILE REFERENCE: 7326-046  
 ; CURRENT APPLICATION NUMBER: US/08/899,232  
 ; CURRENT FILING DATE: 1997-07-23  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 2523  
 ; TYPE: PRT  
 ; ORGANISM: *Xenopus sp.*  
 US-08-899-232-3

Query Match 3.6%; Score 8; DB 2; Length 2523;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 8; Conservative 0; Mismatches 0;  
 Gaps 0;  
 Indels 0;

Qy 91 CRNGGTCV 98  
 Db 265 CRNGGTCV 272

RESULT 5  
 US-09-121-457-3  
 ; Sequence 3, Application US/09121457  
 ; Patent No. 6692919  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Artavanis-Tsakonas, S.  
 ; FILE REFERENCE: 7326-073  
 ; CURRENT APPLICATION NUMBER: US/09/121,457  
 ; CURRENT FILING DATE: 1998-07-23  
 ; EARLIER APPLICATION NUMBER: 08/899,232  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 2523  
 ; TYPE: PRT  
 ; ORGANISM: *Xenopus sp.*  
 US-09-121-457-3

Query Match 3.6%; Score 8; DB 2; Length 2523;  
 Best Local Similarity 100.0%; Pred. No. 85;

Qy 83 GASARPRC 90  
 Db 352 GASARPRC 359

RESULT 3  
 US-08-185-432-18  
 ; Sequence 18, Application US/08185432  
 ; Patent No. 5750552  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Artavanis-Tsakonas, Spyridon  
 ; FILE REFERENCE: Busseau, Isabelle  
 ; APPLICANT: Diederich, Robert J.  
 ; APPLICANT: Xu, Tian  
 ; APPLICANT: Matsuno, Kenji  
 ; TITLE OF INVENTION: DEUTEX PROTEINS, NUCLEIC ACIDS, AND  
 ; COMPOSITIONS  
 ; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/185,432  
 ; FILING DATE: 21-JAN-1994  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mirock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; DOCKET NUMBER: 7326-006

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ; Sequence 3983, Application US/09621976
Qy 91 CRNGTCV 98 ; Patent No. 6639063
Db 265 CRNGTCV 272 ; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
SEQ ID NO 3983
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24..-1
US-09-621-976-3983

RESULT 6
US-09-489-039A-9115
; Sequence 9115, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2799 2004001
; CURRENT FILING DATE: US/09/489,039A
; PRIORITY NUMBER: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9115
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9115

Query Match 3.1%; Score 7; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 175 APSILL 181 ; Sequence 5415, Application US/09621976
Db 8 APSILL 14 ; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
SEQ ID NO 5415
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24..-1
US-09-621-976-5415

RESULT 7
US-09-621-976-5356
; Sequence 5356, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT FILING DATE: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
SEQ ID NO 5356
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17..-1
; NAME/KEY: UNSURE
; LOCATION: 39
; OTHER INFORMATION: Xaa = Ala, Pro
US-09-621-976-5356

Query Match 3.1%; Score 7; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 173 GGAPSL 179 ; Sequence 341, Application US/09149476
Db 60 GGAPSL 66 ; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002PL
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493

RESULT 8
US-09-621-976-3983

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EARLIER FILING DATE: 1997-05-23 ; EARLIER APPLICATION NUMBER: 60/047,589 ; EARLIER FILING DATE: 1997-05-23 ; EARLIER APPLICATION NUMBER: 60/047,593 ; EARLIER FILING DATE: 1997-05-23 ; EARLIER APPLICATION NUMBER: 60/047,614 ; EARLIER FILING DATE: 1997-05-23 ; EARLIER APPLICATION NUMBER: 60/043,578 ; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/043,576 ; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/047,501 ; EARLIER FILING DATE: 1997-05-23 ; EARLIER APPLICATION NUMBER: 60/043,670 ; EARLIER FILING DATE: 1997-04-11 ; EARLIER APPLICATION NUMBER: 60/056,632 ; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,664 ; EARLIER APPLICATION NUMBER: 60/056,876 ; EARLIER APPLICATION NUMBER: 60/056,881 ; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,909 ; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,875 ; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,862 ; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,887 ; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/056,908 ; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/048,964 ; EARLIER FILING DATE: 1997-06-16 ; EARLIER APPLICATION NUMBER: 60/057,650 ; EARLIER FILING DATE: 1997-09-05 ; EARLIER APPLICATION NUMBER: 60/056,884 ; EARLIER FILING DATE: 1997-08-22 ; EARLIER APPLICATION NUMBER: 60/057,669 ; EARLIER FILING DATE: 1997-09-15 ; EARLIER APPLICATION NUMBER: 60/049,610 ; EARLIER FILING DATE: 1997-06-13 ; EARLIER APPLICATION NUMBER: 60/061,060 ; EARLIER FILING DATE: 1997-10-02

Query Match 3.1%; Score 7; DB 2; Length 106; Best Local Similarity 100.0%; Pred. No. 52%; Mismatches 0; Indels 0; Gaps 0;

Qy 175 APSILL 181  
Db 2 APSILL 8

RESULT 11  
US-09-461-325-484  
Sequence 484 Application US/09461325A  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 94 Human Secreted Proteins  
FILE REFERENCE: P2039P1  
CURRENT APPLICATION NUMBER: US/09/461,325A  
CURRENT FILING DATE: 1999-12-14  
EARLIER APPLICATION NUMBER: PCT/US99/13418  
EARLIER FILING DATE: 1999-06-15  
EARLIER APPLICATION NUMBER: 60/089,507  
EARLIER FILING DATE: 1998-06-16  
EARLIER APPLICATION NUMBER: 60/089,508  
EARLIER FILING DATE: 1998-06-16  
EARLIER APPLICATION NUMBER: 60/089,509  
EARLIER FILING DATE: 1998-06-16  
EARLIER APPLICATION NUMBER: 60/089,510  
EARLIER FILING DATE: 1998-06-16  
EARLIER APPLICATION NUMBER: 60/090,112  
EARLIER FILING DATE: 1998-06-22  
EARLIER APPLICATION NUMBER: 60/090,113  
EARLIER FILING DATE: 1998-06-22

Query Match 3.1%; Score 7; DB 2; Length 107; Best Local Similarity 100.0%; Pred. No. 52%; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SILLLP 183  
Db 24 SILLLP 30

RESULT 13

US-10-115-123-484  
 ; Sequence 44, Application US/10115123  
 ; Patent No. 674416  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: 94 Human Secreted Proteins  
 ; FILE REFERENCE: P2039G30AP1D2  
 ; CURRENT APPLICATION NUMBER: US/10/115,123  
 ; CURRENT FILING DATE: 2002-04-04  
 ; PRIOR APPLICATION NUMBER: PCT/US99/13418  
 ; PRIOR FILING DATE: 1999-06-15  
 ; PRIOR APPLICATION NUMBER: 60/089,507  
 ; PRIOR FILING DATE: 1998-06-16  
 ; PRIOR APPLICATION NUMBER: 60/089,508  
 ; PRIOR FILING DATE: 1998-06-16  
 ; PRIOR APPLICATION NUMBER: 60/089,509  
 ; PRIOR FILING DATE: 1998-06-16  
 ; PRIOR APPLICATION NUMBER: 60/089,510  
 ; PRIOR FILING DATE: 1998-06-16  
 ; PRIOR APPLICATION NUMBER: 60/090,112  
 ; PRIOR FILING DATE: 1998-06-22  
 ; PRIOR APPLICATION NUMBER: 60/090,113  
 ; PRIOR FILING DATE: 1998-06-22  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 494  
 ; LENGTH: 107  
 ; TYPE: PRF  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (84)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-115-123-484

Query Match 3.1%; Score 7; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLP 183  
 Db 24 SLLLLP 30

RESULT 14  
 US-09-248-796A-26607  
 ; Sequence 26807, Application US/09248796A  
 ; Patent No. 6747137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keith Weinstock et al.  
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
 ; FILE REFERENCE: 107196.132  
 ; CURRENT APPLICATION NUMBER: US/09/248,796A  
 ; CURRENT FILING DATE: 1999-02-12  
 ; PRIOR APPLICATION NUMBER: US 60/074,725  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 60/096,409  
 ; PRIOR FILING DATE: 1998-08-13  
 ; NUMBER OF SEQ ID NOS: 28208  
 ; SEQ ID NO 26807  
 ; LENGTH: 111  
 ; TYPE: PRF  
 ; ORGANISM: Candida albicans

US-09-248-796A-26607

Query Match 3.1%; Score 7; DB 2; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 ALIHLRL 191  
 Db 75 ALIHLRL 81

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:12:14 ; Search time 169 Seconds  
 (without alignments)  
 611.224 Million cell updates/sec

Title: US-10-665-602-2  
 Perfect score: 223  
 Sequence: 1 MTWRRHVRLLFTVSLAQI...PSVLRQRERRPGRGPGHLR 223

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 6

Total number of hits satisfying chosen parameters: 17010

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*

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2: /EMC\_Celerra\_SDSD3\_Prodata/2/pubpaa/US08\_PUBCOMB.pep:\*

3: /EMC\_Celerra\_SDSD3\_Prodata/2/pubpaa/US09\_PUBCOMB.pep:\*

4: /EMC\_Celerra\_SDSD3\_Prodata/2/pubpaa/US10\_PUBCOMB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	223	100.0	223	4 US-10-665-602-2	Sequence 2, Appli
2	223	100.0	229	3 US-09-764-893-98	Sequence 98, Appli
3	223	100.0	229	3 US-09-764-881-101	Sequence 101, Appli
4	223	100.0	229	3 US-09-763-608	Sequence 608, Appli
5	223	100.0	229	3 US-09-764-898-269	Sequence 269, Appli
6	223	100.0	229	3 US-09-764-881-101	Sequence 101, Appli
7	223	100.0	229	4 US-10-242-747-101	Sequence 98, Appli
8	223	100.0	229	4 US-10-295-027-422	Sequence 101, Appli
9	187	83.9	223	4 US-10-295-027-422	Sequence 422, Appli
10	187	83.9	223	4 US-10-295-027-422	Sequence 129, Appli
11	187	83.9	223	4 US-10-264-237-2712	Sequence 2712, Appli
12	187	83.9	223	5 US-10-940-431-4	Sequence 4, Appli
13	187	83.9	231	3 US-09-764-898-198	Sequence 198, Appli
14	65.0	223	4 US-10-257-113-2	Sequence 2, Appli	
15	6.7	202	5 US-10-940-431-3	Sequence 3, Appli	
16	9	157	4 US-10-125-115-351909	Sequence 351909, Appli	
17	8	3.6	51	4 US-10-424-599-252112	Sequence 252112, Appli
18	8	3.6	51	4 US-10-437-963-124573	Sequence 124573, Appli
19	8	3.6	55	4 US-10-337-963-141814	Sequence 141814, Appli
20	8	3.6	55	4 US-10-425-115-249327	Sequence 249327, Appli
21	8	3.6	85	4 US-10-425-115-267112	Sequence 267112, Appli
22	8	3.6	105	4 US-10-437-963-138083	Sequence 138083, Appli
23	8	3.6	123	4 US-11-096-568A-2904	Sequence 2904, Appli
24	8	3.6	149	6 US-11-096-568A-2904	Sequence 32931, Appli
25	8	3.6	158	6 US-10-167-701-58031	Sequence 58031, Appli
26	8	3.6	170	4 US-10-190-115-63855	Sequence 131, Appli
27	8	3.6	180	3 US-09-860-670-131	Sequence 131, Appli

#### ALIGNMENTS

RESULT 1  
 US-10-665-602-2  
 ; Sequence 2, Application US-10665602  
 ; Publication No. US200400086967A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Meissner, Paul S.  
 ; COLEMAN, Timothy A.  
 ; TITLE OF INVENTION: Human Criptin Growth Factor  
 ; NUMBER OF SEQUNENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: MD  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.3.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US-10-665, 602  
 ; FILING DATE: 22-Sep-03  
 ; CLASSIFICATION: <Unknown>  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US-09/393, 023A  
 ; FILING DATE: 09-SEP-1999  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Marks, Michelle S.  
 ; REGISTRATION NUMBER: 41, 971  
 ; REFILEMENT DOCKET NUMBER: PF200D1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 301-309-8504  
 ; TELEFAX: 301-309-8339  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 223 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: Protein  
 ; 267112 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 ; US-10-665-602-2  
 ; Query Match 100.0%; Score 223; DB 4;  
 ; Best Local Similarity 100.0%; Pred. No. 1.e-196;  
 ; Matches 32931; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MTWRHHYRLFTSLAQINLNQSYQREKHNGRGEVTKVATQKHSPLNTSSHFB 60  
 Database 1 MTWRHHYRLFTSLAQINLNQSYQREKHNGRGEVTKVATQKHSPLNTSSHFB 60  
 Query 61 VTAGSAEGWGPPEPLPYSRAFEGEASAPRCCRNGTCVLSFCVCPAHTGRCYCBHDQRR 120  
 Database 61 VTAGSAEGWGPPEPLPYSRAFEGEASAPRCCRNGTCVLSFCVCPAHTGRCYCBHDQRR 120  
 Query 121 SECGALEHGAWTLRACHLCRCLFGALHCLPLQTPDRCDPKDPLFLASHANGPSAGAPSLL 180  
 Database 121 SECGALEHGAWTLRACHLCRCLFGALHCLPLQTPDRCDPKDPLFLASHANGPSAGAPSLL 180  
 Query 181 LLPCALLHLRLRPAHPRSLVPSVLQERPRPGPGLGHRL 223  
 Database 181 LLPCALLHLRLRPAHPRSLVPSVLQERPRPGPGLGHRL 223  
 Query 181 LLPCALLHLRLRPAHPRSLVPSVLQERPRPGPGLGHRL 223  
 Database 181 LLPCALLHLRLRPAHPRSLVPSVLQERPRPGPGLGHRL 223

**RESULT 2**  
 US-09-764-893-98  
 Sequence 98, Application US/09764893  
 Publication No. US20020086330A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen, et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PJJ209  
 CURRENT APPLICATION NUMBER: US/09/764,893  
 CURRENT FILING DATE: 2001-01-19  
 PRIOR APPLICATION data removed - consult PALM or file wrapper  
 NUMBER OF SEQ ID NOS: 154  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 98  
 LENGTH: 229  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (2)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (3)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-764-893-98  
 Query Match 100.0%; Score 223; DB 3; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-196; Indels 0; Gaps 0;  
 Matches 223; Conservative 0; Mismatches 0;  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (2)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (3)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-764-893-98  
 Query Match 100.0%; Score 223; DB 3; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-196; Indels 0; Gaps 0;  
 Matches 223; Conservative 0; Mismatches 0;  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (2)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (3)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-764-893-98

**RESULT 3**  
 US-09-764-891-101  
 Sequence 101, Application US/09764881  
 Publication No. US20020086821A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen, et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PJJ206  
 CURRENT APPLICATION NUMBER: US/09/764,881  
 CURRENT FILING DATE: 2001-01-17  
 PRIOR APPLICATION data removed - consult PALM or file wrapper  
 NUMBER OF SEQ ID NOS: 939  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 608  
 LENGTH: 229  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (2)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (3)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-764-891-101  
 Query Match 100.0%; Score 223; DB 3; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-196; Indels 0; Gaps 0;  
 Matches 223; Conservative 0; Mismatches 0;  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (2)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: SITE  
 LOCATION: (3)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-764-891-101

RESULT 5  
 US-03-764-898-269  
 ; Sequence 269, Application US/09764898  
 ; Patent No. US20020090673A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; CURRENT APPLICATION NUMBER: US/09/764,898  
 ; CURRENT FILING DATE: 2001-01-17  
 ; NUMBER OF SEQ ID NOS: 311  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO: 269  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (2)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (3)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; US-03-764-898-269

Query Match 100.0%; Score 223; DB 3; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-196;  
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 7 MTWRHHVRLFTSALQIINLGSYQREKNGRGEVTYATOKHRSPLNTSSHFGE 66

Qy 61 VTGSAEGWGPPEEPLPYSRAFEGASARPRCCRNGTCVLSFCVCPAHTGRCYCEHDQRR 120  
 Db 67 VTGSAEGWGPPEEPLPYSRAFEGASARPRCCRNGTCVLSFCVCPAHTGRCYCEHDQRR 126

Qy 121 SECGLAEGWATLRAAHCRCIFGALHCLPLQTPRCDPKDFLASHAHPSPAGAPSLL 180  
 Db 127 SECGLAEGWATLRAAHCRCIFGALHCLPLQTPRCDPKDFLASHAHPSPAGAPSLL 186

Qy 181 LLPCALLHRLRDPAPAHPSLVPSPVTLQERRPGRPGLGHLR 223  
 Db 187 LLPCALLHRLRDPAPAHPSLVPSPVTLQERRPGRPGLGHLR 229

Qy 121 SECGLAEGWATLRAAHCRCIFGALHCLPLQTPRCDPKDFLASHAHPSPAGAPSLL 180  
 Db 127 SECGLAEGWATLRAAHCRCIFGALHCLPLQTPRCDPKDFLASHAHPSPAGAPSLL 186

RESULT 6  
 US-03-764-881-101  
 ; Sequence 101, Application US/09764881  
 ; Publication No. US2003012546A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PT207  
 ; CURRENT FILING DATE: 2001-01-17  
 ; Prior application data removed - refer to PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 192  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO: 101

Query Match 100.0%; Score 223; DB 4; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-196;  
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTWRHHVRLFTSALQIINLGSYQREKNGRGEVTYATOKHRSPLNTSSHFGE 60  
 Db 7 MTWRHHVRLFTSALQIINLGSYQREKNGRGEVTYATOKHRSPLNTSSHFGE 66

Qy 61 VTGSAEGWGPPEEPLPYSRAFEGASARPRCCRNGTCVLSFCVCPAHTGRCYCEHDQRR 120  
 Db 67 VTGSAEGWGPPEEPLPYSRAFEGASARPRCCRNGTCVLSFCVCPAHTGRCYCEHDQRR 126

Qy 121 SECGLAEGWATLRAAHCRCIFGALHCLPLQTPRCDPKDFLASHAHPSPAGAPSLL 180  
 Db 127 SECGLAEGWATLRAAHCRCIFGALHCLPLQTPRCDPKDFLASHAHPSPAGAPSLL 186

Qy 181 LLPCALLHRLRDPAPAHPSLVPSPVTLQERRPGRPGLGHLR 223  
 Db 187 LLPCALLHRLRDPAPAHPSLVPSPVTLQERRPGRPGLGHLR 229

Qy 121 SECGLAEGWATLRAAHCRCIFGALHCLPLQTPRCDPKDFLASHAHPSPAGAPSLL 180  
 Db 127 SECGLAEGWATLRAAHCRCIFGALHCLPLQTPRCDPKDFLASHAHPSPAGAPSLL 186

Db 127 SECAGALEHGAWTLRACHLRCR1FGALHCLPLQTPDRCDKDFLASHAGPSAGGAPSILL 186

Qy 181 LLPCALLHLLRDPDAHPLRSVLVSLQERRPCRGPCGHRL 223

Db 187 LLPCALLHLLRDPDAHPLRSVLVSLQERRPCRGPCGHRL 229

RESULT 8

US-10-242-747-101

Sequence 101, Application US/10242747

Publication No. US20040005577A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PTZ0C1

CURRENT APPLICATION NUMBER: US/10/242,747

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: 09/764,881

PRIOR FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 60/179,065

PRIOR FILING DATE: 2000-01-31

PRIOR APPLICATION NUMBER: 60/180,628

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR FILING DATE: 2000-06-28

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR FILING DATE: 2000-08-14

PRIOR APPLICATION NUMBER: 60/220,963

PRIOR FILING DATE: 2000-07-26

PRIOR APPLICATION NUMBER: 60/217,496

PRIOR FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/225,447

PRIOR FILING DATE: 2000-08-14

PRIOR APPLICATION NUMBER: 60/218,290

PRIOR FILING DATE: 2000-07-14

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 192

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 101

TYPE: PRT

LENGTH: 229

FEATURE: misc\_feature

ORGANISM: Homo sapiens

FEATURE: misc\_feature

NAME/KEY: misc\_feature

LOCATION: (2)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE: misc\_feature

NAME/KEY: misc\_feature

LOCATION: (3)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-242-747-101

Query Match 100.0%; Score 223; DB 4; Length 229;

Best Local Similarity 100.0%; Pred. No. 1.5e-16;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTWRRHVRLLFTVSLAQIINLGNSYQREKHNGGRGEVTKVATOKHROSPWLTSSHFG 60

Db 7 MTWRRHVRLLFTVSLAQIINLGNSYQREKHNGGRGEVTKVATOKHROSPWLTSSHFG 66

Qy 61 VTGSAEGNGPPEEPYPSRAFEGEGASAPCCRNQTCVLSFCYCPAHTGRCYCEHQR 120

Db 67 VTGSAEGNGPPEEPYPSRAFEGEGASAPCCRNQTCVLSFCYCPAHTGRCYCEHQR 126

Qy 121 SECAGALEHGAWTLRACHLRCR1FGALHCLPLQTPDRCDKDFLASHAGPSAGGAPSILL 180

Db 127 SECAGALEHGAWTLRACHLRCR1FGALHCLPLQTPDRCDKDFLASHAGPSAGGAPSILL 186

Qy 181 LLPCALLHLLRDPDAHPLRSVLVSLQERRPCGRPGIGHRL 223

Db 187 LLPCALLHLLRDPDAHPLRSVLVSLQERRPCGRPGIGHRL 229

RESULT 9

US-10-95-057-422

Sequence 422, Application US/10295027

Publication No. US20030232350A1

GENERAL INFORMATION:

APPLICANT: Afar, Daniel

APPLICANT: Afar, Natasha

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Gish, Kurt C.

APPLICANT: Glynn, Richard

APPLICANT: Hevezsi, Peter A.

APPLICANT: Mack, David H.

APPLICANT: Murray, Richard

APPLICANT: Watson, Susan R.

APPLICANT: Bio-Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and Methods of Screening for Modulators of Cancer

FILE REFERENCE: 018501-012500US

CURRENT APPLICATION NUMBER: US/10/295,027

CURRENT FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: US 09/663,733

PRIOR FILING DATE: 2000-09-15

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/335,394

PRIOR FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR FILING DATE: 2002-01-08

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR FILING DATE: 2002-01-10

PRIOR APPLICATION NUMBER: US 60/355,250

PRIOR FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US 60/356,714

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1386

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 422

LENGTH: 223

TYPE: PRT

ORGANISM: Homo sapiens

US-10-295-027-422

Query Match 83.9%; Score 187; DB 4; Length 223;

Best Local Similarity 100.0%; Pred. No. 1.8e-163;

Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 EYTKVATOKHROSPWLTSSHFGEVTSAAEGNGPPEEPYPSRAFEGEGASAPCCRNQTC 96

Db 37 EYTKVATOKHROSPWLTSSHFGEVTSAAEGNGPPEEPYPSRAFEGEGASAPCCRNQTC 96

Qy 97 CYLGIFCVCPAHTGRCYCEHQRSECGALHGTAWTLRACHLRCR1FGALHCLPLQTPDR 156

Db 97 CYLGIFCVCPAHTGRCYCEHQRSECGALHGTAWTDRACHLRCR1FGALHCLPLQTPDR 156

Qy 157 CDPKDFLASHAGPSAGGAPSILLICALLHLLRDAPAHPSVLORERPGR 216

Db 157 CDPKDFLASHAGPSAGGAPSILLICALLHLLRDAPAHPSVLORERPGR 216

Qy 217 PGIGHRL 223

Db 217 PGIGHRL 223

GENERAL INFORMATION:  
 APPLICANT: Biese et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PA131P1  
 CURRENT APPLICATION NUMBER: US/10/264,237  
 CURRENT FILING DATE: 2002-10-04  
 PRIORITY APPLICATION NUMBER: PCT/US01/16450  
 PRIORITY FILING DATE: 2001-05-18  
 PRIORITY APPLICATION NUMBER: US 60/205,515  
 PRIORITY FILING DATE: 2000-05-19  
 NUMBER OF SEQ ID NOS: 2876  
 SOFTWARE: PatentIn Ver. 3.1  
 SEQ ID NO: 2712  
 LENGTH: 223  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-264-237-2712

Query Match 83.9%; Score 187; DB 4; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-163;  
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 37 EYTKVATQKHOQSPNWTSSHGEVTGSAEGNGPEEPLPSRAFGEASARPRCCRNGET 96  
 Db 37 EYTKVATQKHOQSPNWTSSHGEVTGSAEGNGPEEPLPSRAFGEASARPRCCRNGET 96

Qy 97 CYLGSPCVCVCPAHFTGRYCEHDQRSEGALEHGAWTLRACHLRCIFGAHLCLPQTQPR 156  
 Db 97 CYLGSPCVCVCPAHFTGRYCEHDQRSEGALEHGAWTLRACHLRCIFGAHLCLPQTQPR 156

Qy 157 CDPKDFFLASHANGPSAGAPSLLLPCALLHLRDPAPHSVLPSVLSVLRERRPCGR 211  
 Db 157 CDPKDFFLASHANGPSAGAPSLLLPCALLHLRDPAPHSVLPSVLSVLRERRPCGR 211

Qy 217 PGLGHRL 223  
 Db 217 PGLGHRL 223

RESULT 1.2  
 US-10-940-431-4  
 / Sequence 4, Application US/10940431  
 / Publication No. US20050208045A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Val, Wylie  
 / APPLICANT: Harrison, Craig A.  
 / APPLICANT: Gray, Peter C.  
 / TITLE OF INVENTION: Cripo Antagonism of Activin and TGF-  
 / TITLE OF INVENTION: Signaling  
 / FILE REFERENCE: D6525  
 / CURRENT APPLICATION NUMBER: US/10/940,431  
 / CURRENT FILING DATE: 2004-09-14  
 / PRIORITY APPLICATION NUMBER: 60/503,046  
 / PRIORITY FILING DATE: 2003-09-15  
 / NUMBER OF SEQ ID NOS: 6  
 / SEQ ID NO: 4  
 / LENGTH: 223  
 / SOFTWARE: Macintosh OS 10  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / OTHER INFORMATION: amino acid sequence of human Cripto protein  
 US-10-940-431-4

Query Match 83.9%; Score 187; DB 5; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-163;  
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 37 EYTKVATQKHOQSPNWTSSHGEVTGSAEGNGPEEPLPSRAFGEASARPRCCRNGET 96  
 Db 37 EYTKVATQKHOQSPNWTSSHGEVTGSAEGNGPEEPLPSRAFGEASARPRCCRNGET 96

Qy 97 CYLGSPCVCVCPAHFTGRYCEHDQRSEGALEHGAWTLRACHLRCIFGAHLCLPQTQPR 156  
 Db 97 CYLGSPCVCVCPAHFTGRYCEHDQRSEGALEHGAWTLRACHLRCIFGAHLCLPQTQPR 156

Qy 157 CDPKDFFLASHANGPSAGAPSLLLPCALLHLRDPAPHSVLPSVLSVLRERRPCGR 211  
 Db 157 CDPKDFFLASHANGPSAGAPSLLLPCALLHLRDPAPHSVLPSVLSVLRERRPCGR 211

Qy 217 PGLGHRL 223  
 Db 217 PGLGHRL 223

RESULT 11  
 US-10-264-237-2712  
 / Sequence 712, Application US/10964237  
 / Publication No. US200400941A1  
 / Publication No. US200400941A1  
 / Software: PatentIn Ver. 3.1  
 / SEQ ID NO: 2712  
 / LENGTH: 223  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / OTHER INFORMATION: amino acid sequence of human Cripto protein  
 US-10-264-237-2712

Query Match 83.9%; Score 187; DB 4; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-163;  
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 37 EYTKVATQKHOQSPNWTSSHGEVTGSAEGNGPEEPLPSRAFGEASARPRCCRNGET 96  
 Db 37 EYTKVATQKHOQSPNWTSSHGEVTGSAEGNGPEEPLPSRAFGEASARPRCCRNGET 96

; ORGANISM: Homo sapiens  
US-10-257-113-2

Query Match 65.0%; Score 145; DB 4; Length 223;  
Best Local Similarity 100.0%; Pred. No. 7.7e-125;  
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 AFGEAGASARPRCCRNGGTCAVLSFCVPAHFTGRYCEHCDQRRECGALEHGAUTLRACHL 138  
Db 79 AFGEAGASARPRCCRNGGTCAVLSFCVPAHFTGRYCEHCDQRRECGALEHGAUTLRACHL 138

Qy 139 CRCIFALHCDPLQTCDPKDPLASHAHGSAGAPSLLLPCALLHLRLLPDR 198  
Db 139 CRCIFALHCDPLQTCDPKDPLASHAHGSAGAPSLLLPCALLHLRLLPDR 198

Qy 199 PRSLVPSVQLQERRPGRPGLGHL 223  
Db 199 PRSLVPSVQLQERRPGRPGLGHL 223

RESULT 13  
US-09-764-898-198  
; Sequence 198, Application US/09764898  
; Patent No. US20090209073A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P0211  
; CURRENT APPLICATION NUMBER: US/09/764,898  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 311  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 198  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (44)  
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
US-09-764-898-198

Query Match 83.9%; Score 187; DB 3; Length 231;  
Best Local Similarity 100.0%; Pred. No. 1.9e-163; Mismatches 0; Indels 0; Gaps 0;

Qy 37 EVTRVATQKRQSPNWTSSHFGETGSGAGWGPBEPLPSRAFEGASARPRCCRNGGT 96  
Db 45 EVTRVATQKRQSPNWTSSHFGETGSGAGWGPBEPLPSRAFEGASARPRCCRNGGT 104  
; LENGTH: 202  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence of mouse Criptic protein  
US-10-940-431-3

Query Match 6.7%; Score 15; DB 5; Length 202;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 NGGTCAVLSFCVCPA 107  
Db 101 NGGTCAVLSFCVCPA 115

Search completed: September 22, 2006, 19:15:43  
Job time : 171 secs

RESULT 14  
US-10-257-113-2  
; Sequence 2, Application US/10257113  
; Publication No. US200510207293A1  
; GENERAL INFORMATION:  
; APPLICANT: DUCKER, KLAUS  
; TITLE OF INVENTION: CRYPTIC-LIKE SECRETED PROTEIN  
; FILE REFERENCE: MERCK-2519  
; CURRENT APPLICATION NUMBER: US/10/257,113  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: EP 00107142.2  
; PRIOR FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 2  
; LENGTH: 223  
; TYPE: PRT

GenCore version 5.1.9  
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OM protein - protein search, using SW model

Run on: September 22, 2006, 19:13:04 ; Search time 34 Seconds  
(without alignments)  
466.741 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTWRHHVRLIFTVSIALQI.....PSVLRERRPGCGRPGIGHRL 223

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 260401 seqs, 71162236 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1506

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

## Post-processing: Listing first 45 summaries

Database : Published Applications AA New:\*

1: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpa/us09\_new\_pub.pep:\*

2: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpa/us06\_new\_pub.pep:\*

3: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpa/us07\_new\_pub.pep:\*

4: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpa/us08\_new\_pub.pep:\*

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6: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpa/us10\_new\_pub.pep:\*

7: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpa/us11\_new\_pub.pep:\*

8: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpa/usco\_new\_pub.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	8	3.6	105	US-10-449-902-29843
2	8	3.6	105	US-10-449-902-31212
3	8	3.6	105	US-10-449-902-32435
4	8	3.6	112	US-10-449-904-9558
5	8	3.6	149	US-10-953-349-18163
6	8	3.6	186	US-10-449-902-41657
7	8	3.6	209	US-10-953-349-18762
8	8	3.6	349	US-10-449-902-4942
9	8	3.6	721	US-10-449-902-50370
10	8	3.6	721	US-10-449-902-45561
11	8	3.6	721	US-10-449-902-4815
12	8	3.6	788	US-10-530-387-275
13	8	3.6	880	US-10-449-902-41116
14	7	3.1	50	US-11-155-389-716
15	7	3.1	51	US-11-155-389-715
16	7	3.1	52	US-11-155-389-713
17	7	3.1	52	US-11-155-389-714
18	7	3.1	73	US-10-449-902-31162
19	7	3.1	107	US-10-953-349-12304
20	7	3.1	109	US-11-155-389-805
21	7	3.1	112	US-11-155-389-462
22	7	3.1	119	US-10-196-749-140
23	7	3.1	119	US-10-525-116-1106
24	7	3.1	119	US-11-101-116-26
25	7	3.1	119	US-11-376-673-26

## ALIGNMENTS

RESULT 1  
US-10-449-902-29843  
; Sequence 29843, Application US/10449902  
; Publication No. US2006012505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449-902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 29843  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-29843

Query Match 8: DB 6; Length 105;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSULLLP 183  
Db 42 PSULLLP 49

RESULT 2  
US-10-449-902-31212  
; Sequence 31212, Application US/10449902  
; Publication No. US2006012505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449-902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269

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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-3838770
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3.1212
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-31212

Query Match 3.6%; Score 8; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2, 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-10-449-902-32435
Sequence 32435, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-3838770
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 105
TYPE: PRT
ORGANISM: Oryza sativa
; US-10-449-902-32435

Query Match 3.6%; Score 8; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2, 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-449-902-49548
Sequence 49548, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-3838770
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
; US-10-449-902-49548

Query Match 3.6%; Score 8; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2, 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-10-253-349-18763
Sequence 18763, Application US/10953349
Publication No. US2006017345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCING-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 18763
LENGTH: 149
TYPE: PRT
ORGANISM: Glycine max
; US-10-253-349-18763

Query Match 3.6%; Score 8; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 3, 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 3.6%; Score 8; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 3, 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-10-449-902-41657
Sequence 41657, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 41657
LENGTH: 186
TYPE: PRT
ORGANISM: Oryza sativa
; US-10-449-902-41657

Query Match 3.6%; Score 8; DB 6; Length 186;
Best Local Similarity 100.0%; Pred. No. 3, 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 3.6%; Score 8; DB 6; Length 186;
Best Local Similarity 100.0%; Pred. No. 3, 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 3.6%; Score 8; DB 6; Length 186;
Best Local Similarity 100.0%; Pred. No. 3, 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSULLLP 183
Db 73 PSULLLP 80

RESULT 7
US-10-449-902-41657
Sequence 41657, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
; US-10-449-902-41657

Query Match 3.6%; Score 8; DB 6; Length 186;
Best Local Similarity 100.0%; Pred. No. 3, 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 APSILLIL 182
Db 45 APSILLIL 52

RESULT 8
US-10-449-902-41657
Sequence 41657, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCING-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 18763
LENGTH: 149
TYPE: PRT
ORGANISM: Glycine max
; US-10-449-902-41657

Query Match 3.6%; Score 8; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 3, 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LFTVSLAL 17
Db 103 LFTVSLAL 110

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Db 146 ||||| ALLHRRLR 153
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT FILING DATE: US/10/449,902
; PRIORITY APPLICATION NUMBER: US/10/449,902
; PRIORITY FILING DATE: 2003-05-29
; PRIORITY APPLICATION NUMBER: JP 2002-203269
; PRIORITY FILING DATE: 2002-05-30
; PRIORITY APPLICATION NUMBER: JP 2002-383870
; PRIORITY FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 50970
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-50970

RESULT 7
US-10-953-349-18762
; Sequence 18762, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40232
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 18762
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-18762

Query Match 3.6%; Score 8; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 LEFTSIAL 17
Db 163 LEFTSIAL 170
; RESULT 10
; Sequence 45561, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT FILING DATE: US/10/449,902
; PRIORITY APPLICATION NUMBER: US/10/449,902
; PRIORITY FILING DATE: 2003-05-29
; PRIORITY APPLICATION NUMBER: JP 2002-203269
; PRIORITY FILING DATE: 2002-05-30
; PRIORITY APPLICATION NUMBER: JP 2002-383870
; PRIORITY FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 45561
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-45561

Query Match 3.6%; Score 8; DB 6; Length 721;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 185 ALLHRLLR 192
Db 107 ALLHRLLR 114
; RESULT 11
; Sequence 48415, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT FILING DATE: US/10/449,902
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 48415
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-48415

Query Match 3.6%; Score 8; DB 6; Length 349;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 176 PSLLLILP 183
Db 4 PSLLLILP 11
; RESULT 12
; Sequence 50970, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT FILING DATE: US/10/449,902

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; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-2032659
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; SEQ ID NO: 48415
; SOFTWARE: PatentIn Ver. 2.1
; TYPE: PRF
; ORGANISM: Oryza sativa
; SEQ ID NO: 48415

Query Match 3.6%; Score 8; DB 6; Length 788;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 175 APSLILL 182
Db 12 APSLILL 19

Query Match 3.6%; Score 8; DB 6; Length 721;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 185 ALHLRLR 192
Db 107 ALHLRLR 114

RESULT 12
; Sequence 25, Application US/10530187
; Publication No. US20060183120A1
; GENERAL INFORMATION:
; APPLICANT: THE, Bin, Team
; TITLE OF INVENTION: Molecular Subclassification of Kidney Tumors and the Discovery of New Diagnostic Markers
; FILE REFERENCE: 28927-0014
; CURRENT APPLICATION NUMBER: US/10/530,187
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031476
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US 60/415,775
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 275
; LENGTH: 788
; TYPE: PRF
; ORGANISM: homo sapiens
; SEQ ID NO: 18-275

Query Match 3.6%; Score 8; DB 6; Length 788;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 175 APSLILL 182
Db 12 APSLILL 19

RESULT 13
; Sequence 4116, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-2032659
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4116
; LENGTH: 880
; TYPE: PRF
; ORGANISM: Oryza sativa
; SEQ ID NO: 4116
; LENGTH: 880
; Score 8; DB 6;
; Best Local Similarity 100.0%; Pred. No. 15;
; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 169 GPSAGGAP 176
Db 398 GPSAGGAP 405

RESULT 14
; Sequence 716, Application US/11155989
; Publication No. US20060177831A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Saniyeve
; APPLICANT: Alba, Benjamin M.
; APPLICANT: Bakker, Alice
; APPLICANT: Duguay, Amy N.
; APPLICANT: Liu, Qiang
; APPLICANT: Silverman, Richard
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001410US
; CURRENT APPLICATION NUMBER: US/11/155,989
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/871,502
; PRIOR FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 10/957,351
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 925
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 716
; LENGTH: 50
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: c-Met-binding family 9 (Fam9)
US-11-155-989-716

Query Match 3.1%; Score 7; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 214 CGRPGLG 220
Db 38 CGRPGLG 44

RESULT 15
; Sequence 715, Application US/11155989
; Publication No. US20060177831A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Saniyeve
; APPLICANT: Alba, Benjamin M.
; APPLICANT: Bakker, Alice
; APPLICANT: Duguay, Amy N.
; APPLICANT: Liu, Qiang
; APPLICANT: Silverman, Richard
; APPLICANT: Smith, Richard
; APPLICANT: Avidia Research Institute
; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001410US
; CURRENT APPLICATION NUMBER: US/11/155,989
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/871,502
; PRIOR FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 10/957,351
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 925
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 715
; LENGTH: 50
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: c-Met-binding family 9 (Fam9)
US-11-155-989-715

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1 TITLE OF INVENTION: c-Met Kinase Binding Proteins  
1 FILE REFERENCE: 022013-0014100S  
1 CURRENT APPLICATION NUMBER: US11/155,989  
1 CURRENT FILING DATE: 2005-06-17  
1 PRIORITY NUMBER: US 10/871,602  
1 PRIORITY FILING DATE: 2004-06-17  
1 PRIORITY APPLICATION NUMBER: US 10/957,351  
1 PRIORITY FILING DATE: 2004-09-30  
1 NUMBER OF SEQ ID NOS: 925  
1 SOFTWARE: FastSEQ for Windows Version 3.0  
1 SEQ ID NO: 715  
1 LENGTH: 51  
1 TYPE: PRF  
1 ORGANISM: Artificial Sequence  
FEATURE:  
1 OTHER INFORMATION: c-Met-binding family 9 (Fam9)  
FEATURE:  
1 NAME/KEY: MOD RES  
1 LOCATION: (17) .. (17)  
1 OTHER INFORMATION: Xaa = any amino acid  
US-11-155-989-715

Query Match 3.1%; Score 7; DB 7; Length 51;  
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Matches 7; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
Qy 214 CGRPGLG 220  
Db 38 CGRPGLG 44

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Job time : 36 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.9	T-cell surface gly
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Title: US-10-665-602-2		hypothetical prote
Perfect score: 223		manganese peroxida
Sequence: 1 MTWRHHVRLFTVSLAQII.....PSVLRERRPGRPGLGHRL 223		hypothetical prote
Scoring table: OLIGO	Gappp 60.0 , Gapext 60.0	Fl4M2.7 protein -
Searched: 283416 seqs, 96216763 residues	Word size : 6	citrate synthase-1
	Total number of hits satisfying chosen parameters: 1138	citrate synthase-1
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Maximum DB seq length: 2000000000		cytochrome-c oxida
Post-processing: Listing first 45 summaries		cytochrome-c oxida
Database : PIR 80.0*		cytochrome-c oxida
	1: Pir1;*	conserved hypothet
	2: Pir2;*	cytochrome-c oxida
	3: Pir3;*	conserved hypothet
	4: Pir4;*	cytochrome-c oxida
		monoamine transpor
		ALIGMENTS
		RESULT 1
		A72770
		hypothetical protein APE0148 - Aeropyrum pernix (strain K1)
		C;Species: Aeropyrum pernix
		C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Sep-2000
		C;Accession: A72770
		R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jir-no, K.; Takah
		awa, H.; Takanishi, M.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K
		DNA Res. 6, 83-101, 1999
		A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
		A;Reference number: A72450; PMID:99310339; PMID:10382566
		A;Status: preliminary
		A;Molecule type: DNA
		A;Residues: 1-162 <KAW>
		A;Cross-references: UNIPARC:UPI000005DA13; DDBJ:AP000058; NID:95103388; PIDN:BA079059.1;
		A;Experimental source: strain K1
		C;Genetics:
		A;Gene: APE0148
		C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0024
		Query Match 3.6%; Score 8; DB 2; Length 162;
		Best Local Similarity 100.0%; Pred. No. 3.0;
		Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		Qy 14 SLALQIIN 21
		Db
		4 SLALQIIN 11
		RESULT 2
		origin-binding protein - bovine herpesvirus 1
		C;Species: bovine herpesvirus 1
		C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004
		C;Accession: S61246
		R;Vlcek, C.; Benes, V.; Lu, Z.; Kutish, G.F.; Paces, V.; Rock, D.; Letchworth, G.J.; Sch
		submitted to the EMBL Data Library, January 1995
		A;Description: Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus
		A;Reference number: S61233
		A;Accession: S61246
		A;Status: preliminary
		A;Molecule type: DNA
		A;Residues: 1-859 <VLIC>
		A;Cross-references: UNIPROT:P52377; UNIPARC:UPI000130B97;
		C;Superfamily: varicella-zoster virus gene 51 protein
		Query Match 3.6%; Score 8; DB 2; Length 859;
		Best Local Similarity 100.0%; Pred. No. 15;
		Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		Qy 185 ALLHLRLR 192

Db 198 ALLBLRL 205

## RESULT 3

A3844 Xoch protein - African clawed frog  
 C;Species: *Xenopus laevis* (African clawed frog)  
 C;Date: 12-Oct-1990 #sequence\_revision 12-Oct-1990 #text\_change 05-Oct-2004  
 C;Accession: A35844  
 R;Coffman, C.; Harris, W.; Kintner, C.  
 A;Title: Xoch, the *Xenopus* homolog of *Drosophila* notch.  
 A;Reference number: A35844; MUID:90385285; PMID:2402639  
 A;Accession: A35844  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-2524 <COP>  
 A;Cross-references: UNIPARC:UPI00004F253  
 C;SuperFamily: notch protein; ankyrin repeat homology; EGF homology  
 C;Keywords: transmembrane protein <EGF2>  
 F;146-177/Domain: EGF homology <EGX1>  
 F;184-215/Domain: EGF homology <EGF1>  
 F;222-254/Domain: EGF homology <EGF>  
 F;456-487/Domain: EGF homology <EGX2>  
 F;557-788/Domain: EGF homology <EGF3>  
 F;1025-1056/Domain: EGF homology <EGX3>  
 F;1924-1956/Domain: ankyrin repeat homology <AN1>  
 F;1957-1989/Domain: ankyrin repeat homology <AN2>  
 F;1991-2023/Domain: ankyrin repeat homology <AN3>  
 F;2024-2056/Domain: ankyrin repeat homology <AN4>  
 F;2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match 3.6%; Score 8; DB 2; Length 2524;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 CRNGTCV 98

Db 266 CRNGTCV 273

## RESULT 4

PH1333 19 heavy chain DJ region (clone Q238-133) - human (fragment)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1333  
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A;Title: Predominance of fetal type DNA Joining in young children with B precursor lymph  
 A;Reference number: PH1302; MUID:93094761; PMID:1460419  
 A;Accession: PH1333  
 A;Molecule type: DNA  
 A;Cross-references: UNIPARC:UPI000017C236  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 3.1%; Score 7; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 7.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLPLP 183

Db 8 SLLLPLP 14

## RESULT 5

AF293 hypothetical protein YP02405 [imported] - *Yersinia pestis* (strain C092)  
 C;Species: *Yersinia pestis*  
 C;Accession: AF293  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-104 <PAR>  
 A;Cross-references: UNIPARC:UPI0000059BFD; GB:AL513382; PMID:916503388; C  
 C;Genetics:

RESULT 6

AF1928 hypothetical protein asl0977 [imported] - *Nostoc* sp. (strain PCC 7120)

C;Species: *Nostoc* sp. PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C;Accession: AF1928  
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, S.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120  
 A;Reference number: AB1807; MUID:21595285; PMID:11759840  
 A;Accession: AF1928  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-76 <KUR>  
 A;Cross-references: UNIPROT:Q8VY74; UNIPARC:UPI00000CDF33; GB:BA000019; PMID:17759840  
 A;Experimental source: strain PCC 7120  
 A;Gene: asl0977

Query Match 3.1%; Score 7; DB 2; Length 76;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 LLLLPLC 184

Db 8 LLLLPLC 14

RESULT 7

AI0775 conserved hypothetical protein yohN [imported] - *Salmonella enterica* subsp. *enterica* serovar *Typhi*

C;Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*  
 A;Note: this species has also been called *Salmonella typhi*  
 C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C;Accession: AI0775  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Churcher, S.; T. Connerton, P.; Cronin, A.; Davies, P.; Quail, M.; Simmonds, M.; Skelton, J.; Stevens, K.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Gaora, P.  
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar *Typhi*  
 A;Reference number: AB0502; MUID:21534947; PMID:11677608  
 A;Accession: AI0775

Query Match 3.1%; Score 7; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 7.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLPLP 183

Db 8 SLLLPLP 14



C;Accession: F64896  
R;Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
A;Cross-references: UNIPROT:Q8X9M4; UNIPARC:UPI00000000789; GB:BA000007; PIDN:BA035470.1;  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of *Escherichia coli* K-12.  
A;Reference number: A61720; MUID:9742617; PMID:9278503  
A;Accession: F64896  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-264 <HAY>  
A;Cross-references: UNIPROT:P77505; UNIPARC:UPI000011A92F; GB:AE000241; GB:U00096; NID:9  
A;Experimental source: strain K-12, substrate MG1655  
C;Superfamily: spermidine/putrescine transport system permease protein potI  
C;Keywords: inner membrane; transmembrane protein  
F;17-33/Domain: transmembrane #status predicted <TM>  
F;100-116/Domain: transmembrane #status predicted <TM3>  
F;133-149/Domain: transmembrane #status predicted <TM4>  
F;186-202/Domain: transmembrane #status predicted <TM5>  
F;237-253/Domain: transmembrane #status predicted <TM6>  
Query Match 3.1%; Score 7; DB 2; Length 264;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
Qy 177 SLILLP 183  
Db 102 SLILLP 108  
RESULT 13  
H8733  
probable transport system permease protein Z2276 [imported] - *Escherichia coli* (strain C  
C;Species: *Escherichia coli*  
C;Accession: H8733  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A;Reference number: A85480; MUID:11206551  
A;Accession: H8733  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-264 <STO>  
A;Cross-references: UNIPROT:Q8X9M4; UNIPARC:UPI00000000789; GB:AE005174; NID:912515259; F  
A;Experimental source: strain O157:H7, substrate EDL933  
C;Genetics:  
A;Gene: 22276  
C;Superfamily: spermidine/putrescine transport system permease protein potI  
Query Match 3.1%; Score 7; DB 2; Length 264;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
Qy 177 SLILLP 183  
Db 102 SLILLP 108  
Search completed: September 22, 2006, 19:01:00  
Job time : 41 secs

RESULT 14  
G90884  
probable transport system permease protein ECB2047 [imported] - *Escherichia coli* (strain C  
C;Species: *Escherichia coli*  
C;Accession: G90884  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Sakawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen  
A;Accession: G90884  
A;Status: preliminary